

Run on: April 15, 2003, 00:14:43 ; Search time 368 413 Seconds
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GenCore version 5.1.4.P5-4578

On nucleic - nucleic search, using sw model

Title: US-09-001-737-7_COPY_15_1652
 Perfect score: 1618
 Sequence: 1 ATGGCAGAAGAATTCATT..... TGGTGGGATGGCGGATAA 1638

Scoring-table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Genesed_101003:*

1: /SIDS2/gcadata/geneseq/geneseq - amb1/NA1980.DAT:*

2: /SIDS2/gcadata/geneseq/geneseq - amb1/NA1981.DAT:*

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44: /SIDS2/gcadata/geneseq/geneseq - amb1/NA2023.DAT:*

45: /SIDS2/gcadata/geneseq/geneseq - amb1/NA2024.DAT:*

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1618	0.000	1661	20	AXX6155	DNA encoding a Str
2	1620	98.9	1635	24	ABN6160	Streptococcus Poly
3	1413.4	86.3	2683	22	ABH5861	S. Pyogenes group
4	1104.4	69.6	1306	22	AAH5862	Antibiotic resista
5	1122.6	68.5	1305	22	AAH5863	Antibiotic resista
6	1062.4	64.9	1620	24	ABN6150	Streptococcus poly
7	1062.4	64.9	215561	24	ABN7152	Streptococcus poly
8	1039.2	63.4	1623	22	AAH98807	Cysteine proteinase
9	1038.4	63.4	1926	22	AAF25036	Nucleotide sequenc

10	1038	63.4	1654	20	AXX86153	DNA encoding a StcFEE 104 coding s.
11	1036	63.2	1647	22	AAH0906	Antibiotic resist.
12	1036	63.2	2107	22	AAH5860	Streptococcus pneumoniae gro.
13	1034.4	63.2	565	19	AN5220	S. pneumoniae gro.
14	1028.6	62.9	2401	22	AAH5859	Genomic sequence.
15	951.2	50.3	2365589	24	ABD0521	Enterococcus faecalis.
16	942.6	57.5	3625	20	AXX12979	Listeria monocytogenes.
17	831.2	50.7	1601	24	ABD0705	Staphylococcus aureus.
18	823.2	50.3	21351	24	ABD07193	S. aureus RN4220.
19	785.4	47.9	1957	22	AAH5686	Methicillin resist.
20	772	47.1	1938	22	AAH5867	Listeria monocytogenes.
21	760.6	46.4	1570	24	ABD09121	S. epidermidis opp.
22	755.4	46.1	1620	22	AAH52698	S. epidermidis gen.
23	755.4	46.1	3185	22	AAH54519	Staphylococcus ep.
24	734.6	44.8	1623	24	ABD09120	S. aureus groE op.
25	721.4	44.0	2712	22	AAH56866	Lawsonia intracellularis.
26	704.2	43.0	1647	18	AAH59201	Genomic fragment.
27	704.2	43.0	4972	18	AAH69203	Buchnera sp. genome.
28	654.2	39.9	96109	22	AAH28548	Antibiotic resist.
29	615.8	37.6	64081	24	ABD92787	Escherichia coli.
30	608.2	37.1	613	22	AAH56864	Escherichia coli O157:H7.
31	604.2	36.9	609	22	AAH56863	DNA encoding a StcFEE 104 coding s.
32	599.8	36.0	1647	22	AAH48498	Multidrug resistance.
33	589.8	36.0	1647	24	ABD90804	Neisseria meningitidis.
34	589.8	36.0	1647	24	ABD93204	Neisseria meningitidis.
35	589.8	36.0	1741	22	AAH56839	Neisseria meningitidis.
36	589.8	36.0	2155	24	AAH33423	Neisseria meningitidis.
37	589.8	36.0	4324	21	AAH48500	Neisseria meningitidis.
38	587.6	35.9	1665	20	AAH86132	Neisseria meningitidis.
39	583.4	35.6	2032	22	AAH56837	Neisseria meningitidis.
40	577.2	35.2	2006	22	AAH66154	Neisseria meningitidis.
41	565.2	34.5	1662	20	AAH66154	Neisseria meningitidis.
42	552.8	34.5	1635	21	AAH54509	Neisseria meningitidis.
43	550	33.6	2465	12	AAH01316	HYP operon. Chlamydia trachomatis.
44	549.8	33.6	91015	20	AAH20200	Neisseria meningitidis.
45	536.8	32.8	1635	21	AAH13000	Neisseria meningitidis.
ALIGNMENTS						
RESULT 1						
AA86155						
ID	AA86155	standard; DNA; 1661 BP.				
XX						
AC	AA86155;					
XX						
DT	22-SEP-1999	(first entry)				
XX						
DE	DNA encoding a Streptococcus pyogenes heat shock protein (Hsp)60-2.					
XX						
KW	Heat shock protein; Hsp60-2; immune response; immunological carrier; cancer control; tumour; sarcoma; cancer; gene therapy; ss.					
XX						
OS	Streptococcus pyogenes.					
XX						
PN	W09935270-A1.					
XX						
PD	15-JUL-1999.					
XX						
PF	29-DBC-1998;	98WO-CA01203.				
XX						
PR	31-DEC-1997;	97US-0001737.				
XX						
PA	(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.					
XX						
PT	Mizzen L, Wisniewski J;					
XX						
DR	WPI: 1999-430397/36.					
XX						
DR	P-PSDB; AAY23904.					
PT	New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer					

agents and for diagnosis

PT

XX

PS

XX

CC

DE Streptococcus polynucleotide SEQ ID NO 6233.
 XX
 XX Streptococcus; G/S; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; anti-bacterial; gene;
 anti-inflammatory; infection; vaccine; meningitis; gene therapy; ds.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PR 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0026727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON S.A.
 (GENO-) INST GENOMIC RES.
 XX
 PI Telford J., Nasiriany V., Margarit Ros YI., Grandi G., Fraser C.;
 PI Tettein H.
 XX
 WP1: 2002-352536738.
 DR P-PSDB; ABP20529.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 or disease caused by Streptococcus bacteria, such as meningitis, and
 for detecting compound that binds to the protein.
 XX
 PS Claim 7; Page 3785-3786; 4525PP; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP1095) from group B
 streptococcus/gas (Streptococcus agalactiae) or group A streptococcus/gas
 (Streptococcus pyogenes), comprising one or of 5483 sequences (S1), given in
 the specification. The proteins have antibacterial and anti-inflammatory
 activity. (I), nucleic acids encoding (I), ABN66044 ABN1556 and
 antibodies that bind (I) are used in the manufacture of medicaments for
 the treatment or prevention of infection or disease caused by
 Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 biological sample. (I) is used to determine whether a compound binds to
 (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 used as a vaccine or diagnostic composition. The disease caused by
 Streptococcus that is prevented or treated may be meningitis. Nucleic
 acid encoding (I) may be used to recombinantly produce (I) and may be
 used in gene therapy. Antibodies to (I) are used for affinity
 chromatography, immunoassays, and distinguishing/identifying
 Streptococcus proteins.
 CC
 XX
 SQ Sequence 1635 BP; 504 A; 303 C; 397 G; 431 T; 0 other;
 XX
 Query Match 98.9%; Score 1670.2; DB 24; Length 1635;
 Best Local Similarity 99.8%; Pred. No:0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1622; Conservative 0;
 QY 1 ATGGCAAAGAGTCAATTTCAGAGATGCCGCTGCTCCATGGCGCGGAGTGTATG 60
 Db 7 ATGGCAAAGAGTCAATTTCAGAGATGCCGCTGCTCCATGGCGCGGAGTGTATG 66
 QY 61 ATGGCAAAGAGTCAATTTCAGAGATGCCGCTGCTCCATGGCGCGGAGTGTATG 120
 Db 67 ATGGCAAAGAGTCAATTTCAGAGATGCCGCTGCTCCATGGCGCGGAGTGTATG 126
 QY 121 AACGCTTGTGTCGCCCTTAATCTAATGAGGGTAACTTGTAAAGGAGTGTGAA 180
 Db 127 AACGCTTGTGTCGCCCTTAATCTAATGAGGGTAACTTGTAAAGGAGTGTGAA 186
 QY 181 TAGAGAGATCATTTGAAACATGGGAGAAATGGTGTGAGAAGGGCTCTAACACC 240
 Db 187 TAGAGAGATCATTTGAAACATGGGAGAAATGGTGTGAGAAGGGCTCTAACACC 246
 QY 241 ATGATATTTCTGTGAGGGACGACTCTGCAACAGTTTGACACAGCTTGTGCA 300
 Db 247 ATGATATTTCTGTGAGGGACGACTCTGCAACAGTTTGACACAGCTTGTGCA 306
 QY 301 GAAGGACTTAAAGATGGAGCAGGGTCTTAACTGCAATGTTGATCGTGGAGGCATGAA 360
 Db 307 GAAGGACTTAAAGATGGAGCAGGGTCTTAACTGCAATGTTGATCGTGGAGGCATGAA 366
 QY 361 ACNGCACACAGCAGGTGAGGCTTGACAGCATGCTCACCTGACAGCAACCCATGTC 420
 Db 367 ACAGCAGCACAGCAGCTGAGGCTTGACAGCATGCTCACCTGATCGTGTGGAGG 426
 QY 421 GAAGCATTGCTCAGGCGCAGCTGAGTACATCACCCTCGAGAAAGTGGAGGTATC 480
 Db 427 GAAGCATTGCTCAGGCGCAGCTGAGTACATCACCCTCGAGAAAGTGGAGGTATC 486
 QY 481 TCGAAGACTTGGGCTGTCAGGCTGAGCAGCTGAGTACATCAGGAGTACCCATCGAGA 540
 Db 487 TCGAAGACTTGGGCTGTCAGGCTGAGCAGCTGAGTACATCAGGAGTACCCATCGAG 546
 QY 541 ATGGAAACAGAACATGAGTGGTGAAGGCGTACCGTACCTGAAAGTGGAGGTATC 600
 Db 547 ATGGAACAGAACATGAGTGGTGAAGGCGTACCGTACCTGAAAGTGGAGGTATC 606
 QY 601 TACATGGTCACAGACAAATGAGAAAATGGTGGAGCATCCACCTGTC 660
 Db 607 TACATGGTCACAGACAAATGAGAAAATGGTGGAGCATCCACCTGTC 666
 QY 661 ACCGATTAAGTGTCAACATCCAGAACATTGCGACACTTGAGGACTCTAA 720
 Db 667 ACCGATTAAGTGTCAACATCCAGAACATTGCGACACTTGAGGACTCTAA 726
 QY 721 ACCAACGGCCATTAATCTCTTATGAGATGAGTGGGAGCTGAAACCCATTCTCA 780
 Db 727 ACCAACGGCCATTAATCTCTGAGATGAGTGGGAGCTGAAACCCATTCTCA 786
 QY 781 GATCTTACAGATGCTGACTCTGAGATGAGTGGGAGCTGAAACCCATTCTCA 840
 Db 787 GATCTTACAGATGCTGACTCTGAGATGAGTGGGAGCTGAAACCCATTCTCA 846
 QY 841 GATCTTACAGATGAGTGGGAGCTGAAACCCATTCTCA 900
 Db 847 GATCTTACAGATGAGTGGGAGCTGAAACCCATTCTCA 906
 QY 901 GAGGACTTGTGACTGTGAAAGATGCTACATGAGCCTTGAGCAGGTGCTAG 960
 Db 907 GAGGACTTGTGACTGTGAAAGATGCTACATGAGCCTTGAGCAGGTGCTAG 966
 QY 961 ATTACAGTGTAAAGATGCTACAGCTGAGTGTGAGGTTGGAGGTCAGACGTT 1020
 Db 967 ATTACAGTGTAAAGATGCTACAGCTGAGTGTGAGGTTGGAGGTCAGACGTT 1026
 QY 1021 GCTAACGGTTGCACTGATAATCCGAACTTAACTGAGCAACACCTCTGACGGT 1080
 Db 1027 GCTAACGGTTGCACTGATAATCCGAACTTAACTGAGCAACACCTCTGACGGT 1086
 QY 1081 GAGAAACTTACAGACACTTGGCAAAATTACTCTGCTGCTGCTGCTGCTGCTG 1140
 Db 1087 GAGAAACTTACAGACACTTGGCAAAATTACTCTGCTGCTGCTGCTGCTG 1146
 QY 1141 GCTCCACAGACAGCTTAAAGAAAGTGAACCTGCTGCTGCTGCTGCTGCTG 1200
 Db 1147 GCTCCACAGACAGCTTAAAGAAAGTGAACCTGCTGCTGCTGCTGCTGCTG 1206
 QY 1201 ACAGCAGCAGCTTGGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 Db 1207 ACAGCAGCAGCTTGGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1266
 QY 1261 ATGAAAGATGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1320
 Db 1267 ATGAAAGATGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1326
 QY 1321 CTTCGCTCTAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1380

Db	1327	CTTCGRCGCTAGAGAGGCCGCTAGTCGAATGCTTAATCTGGTAGAGGGCTCC	1386
Oy	1381	GGATGATGACAGTCAGGAAACGGCCCTGGAGGACAGATTTAGCAGCACAGGT	1440
Db	1387	GTGATGATTGACAGTGTGAAACAGCCGCTGGAGGACAGATTTAGCAGCACAGGT	1446
Oy	1441	GAGTGGTGTGATGATGAAACAGGAACTATGACGCCGCTGGAGGACAGATTTAGCAGCACAGGT	1500
Db	1447	GAGTGGTGTGATGATGAAACAGGAACTATGACGCCGCTGGAGGACAGATTTAGCAGCACAGGT	1506
Oy	1501	CTTCAAAGGCGAGCTTGCTGAGCTGTCTTAATTGACACAGACAGCAGTTGAGCTAT	1560
Db	1507	CTTCAAAGGCGAGCTTGCTGAGCTGTCTTAATTGACACAGACAGCAGTTGAGCTAT	1566
Oy	1561	AAACCTGGAAACCTGGCCAGCGCCAGCACTGCGAGCAGTTGGATCCAGGATGATG	1620
Db	1567	AACTGGCCCTGGCCAGCGCCAGCACTGCGAGCAGTTGGATCCAGGATGATG	1626

inhibiting expression of GL or GS in cells or tissues in vitro. (1) are also useful for inhibiting the growth of a microorganism, or inhibiting the expression of GL or GS gene in a microorganism (a bacterium or a virus) having a GL or GS gene which involves administering to the microorganism or to a cell infected with the microorganism, (1). (1) are also useful for treating a mammalian pathological condition mediated by the microorganisms which involves identifying a eukaryotic organism having a pathological condition mediated by microorganisms having a GL or GS gene and administering (1) such that the growth of microorganism is inhibited. The antisense compounds are utilized for diagnostics, therapeutics, prophylaxis and as research reagents and kits, e.g., to prevent or delay microbial infections in humans. They are also useful as molecular weight markers. AAK56562 to AAK56367 and AAK5633 to AAK56854 represent PCR primers for grot sequences which are used in the exemplification of the present invention. AAK56855 to AAK56870 represent gross nucleotide sequence given in the present invention.

CC	inhibiting expression of GL or GS in cells or tissues in vitro. (I) are also useful for inhibiting the growth of a microorganism, or inhibiting the expression of GL or GS gene in a microorganism (a bacterial cell or a virus), having a GL or GS gene which involves administering to the microorganism or to a cell infected with the microorganism. (II). (I) are also useful for treating a mammalian pathological condition mediated by the microorganisms which involves identifying a eukaryotic organism having a pathological condition mediated by microorganisms having a GL or GS gene and administering (I) such that the growth of microorganism is inhibited. The antisense compounds are utilised for diagnostics, therapeutics, prophylaxis and as research reagents and kits, e.g., to prevent or delay microbial infections in humans. They are also useful as molecular weight markers. AAH5652 to AAH5637 and AAH5633 to AAH5654 represent PCR primers for grot sequences which are used in the exemplification of the present invention. AAH6853 to AAH56870 represent grot nucleotide sequence given in the present invention.
CC	Query Match: 2683 BP; 808 A; 490 C; 593 G; 792 T; 0 other;
CC	Best Local Similarity: 96.3%; Score: 1413.4; DB: 22; Length: 2683;
CC	Matches: 1423; Conservative: 98.9%; Pred. No.: 0; Mismatches: 16; Indels: 0; Gaps: 0;
OY	187 GATCATTGAAACATGGAGGAATTGGCTGAGGGCTCAACCATGAT 246
Db	1 GATCATTGAAACATGGAGGAATTGGCTGAGGGCTCAACCATGAT 60
OY	247 AATGCTGGTATGGAGCACTACTGCACAGTTGACACAGCCATGTCATGAGGA 306
Db	61 AATGCTGGTATGGAGCACTACTGCACAGTTGACACAGCCATGTCATGAGGA 120
OY	307 CTAAAAATGTACACAGCAGGTTGTAATCCATGGTGTGTTGACAGCCATGTCATGAGGA 366
Db	121 CTAAAAATGTACACAGCAGGTTGTAATCCATGGTGTGTTGACAGCCATGTCATGAGGA 180
OY	367 ACACGACAGCCTGTCAGCCAGCTTGTGAAAGCCATGCTAACCTGTATCTGGAGGAGCT 426
Db	181 ACACGACAGCCTGTCAGCCAGCTTGTGAAAGCCATGCTAACCTGTATCTGGAGGAGCT 240
OY	427 ATTCGTCAGTGGCTCACTATCATCGCTCAGGAAAGTGGAGATACGAGCTGAAAGTGGAGATACGAGCT 486
Db	241 ATTCGTCAGTGGCTCACTATCATCGCTCAGGAAAGTGGAGATACGAGCTGAAAGTGGAGATACGAGCT 300
OY	487 GCTATGGAGCGTGGGGCACATGGTGTGATPACCATGGAGATACGAGCTGGAGGATGGAA 546
Db	301 GCTATGGAGCGTGGGGCACATGGTGTGATPACCATGGAGATACGAGCTGGAGGATGGAA 360
OY	547 ACAGACTTGTGGTGAAGCCATGCAATTGGACCGTGTGTTACCTGCTCAATACATG 606
Db	361 ACAGACTTGTGGTGAAGCCATGCAATTGGACCGTGTGTTACCTGCTCAATACATG 420
OY	607 GTCACAGACAATGAAAAATGGTGTGAGACCTGTAAGAACCCATTACTTAAATCAGGAT 666
Db	421 GTCACAGACAATGAAAAATGGTGTGAGACCTGTAAGAACCCATTACTTAAATCAGGAT 480
OY	667 AAAAGAGCTCACATCCAAAGCATTTGGCAACTACTTGAGGAATGGCTTAACACAC 726
Db	481 AAAAGAGCTCACATCCAAAGCATTTGGCAACTACTTGAGGAATGGCTTAACACAC 540
OY	727 CGTCATCATTCATTATGCAAGTATGGAGGAGAACCTCCACCTGCTG 786
Db	541 CGTCATCATTCATTATGCAAGTATGGAGGAGAACCTCCACCTGCTG 600
OY	787 AACAGAGCTGGTACTTCATGGCTGCTGTAAGCCGAGATTTGGGATGCT 846
Db	601 AACAGAGCTGGTACTTCATGGCTGCTGTAAGCCGAGATTTGGGATGCT 660
OY	847 CGTAAAGCTATGGCTGAGACATGCTATCTGAGGGCTGACAGGATGCTACAGGATGAGGAT 906
Db	661 CGTAAAGCTATGGCTGAGACATGCTATCTGAGGGCTGCTACAGGATGAGGAT 720
OY	907 CTGAGCTGTGATTAAGAGTGTCTCAATGAGAGCCCTGGAGAGGGTGTGATGATCA 966

Db	721 CTAGGACTGATTAAAGATGTTACATGACAGCCCTGGACAGCTGCTAGATATACA	780	PA (GENE-) GENESENSE TECHNOLOGIES INC.
OY	967 GTTGATAAAGATGACAGCACTAATGTTGAAAGGTCAGCAACTTGAGCTATTCAC	1026	XX
Db	781 GTTGATAAAGATGACAGCACTAATGTTGAAAGGTCAGCAACTTGAGCTATTCAC	840	PI Wright JA, Young AH, Dugourd D;
OY	1027 CTATGCACTGATTAAATGCACTTGAAGACACAACTTGACTTGACCTTGACCTTG	1086	XX DR WPI: 2001-355633/37.
Db	841 CCATGCACTTAAATGCACTTGAAGACACAACTTGACCTTGACCTTGACCTTG	900	PT Novel antisense compounds targeting nucleic acid encoding groE or
OY	1087 CTACAGAGACGTTGGCAATTAGCTGTTAGCTGTTAGCTGTTAGCTGTTAGCTG	900	PT expression of the genes, useful to inhibit growth of microorganism
Db	901 CTACAGAGACGTTGGCAATTAGCTGTTAGCTGTTAGCTGTTAGCTGTTAGCTG	960	PT having the genes
OY	1147 ACAGAGACGCTTAAGAAGAACTTGCACTGAGGAGCTTAATGCTACAGCT	1206	XX Disclosure: Fig 8; 110pp; English.
Db	961 ACAGAGACGCTTAAGAAGAACTTGCACTGAGGAGCTTAATGCTACAGCT	1206	CC The present invention specifically claims AAH56368 to AAH56832 which are
OY	1207 GCAGCGTGTGAGAAGGTATCTGCTGGGGGAGACACTTACGGTTAGTAA	1266	CC antisense oligonucleotides to nucleotide sequences encoding groE. More
Db	1021 GCAGCGTGTGAGAAGGTATCTGCTGGGGGAGACACTTACGGTTAGTAA	1080	CC generally, antisense compounds (I) comprising antisense oligonucleotides
OY	1327 GCTCTAGAGAGGCTTGAGCTGAGTCATAATTGCTTAACTGCTGTTAGCTG	1386	CC of 5-50 bases targeted to a nucleotide sequence encoding groE (heat
Db	1267 AAAGTAGAGCTCTGAGCTTAAAGAAACTTGCACTGAGGAGCTTAA	1326	CC shock protein (HSP160) (GL) and groS (HSP10) (GS) gene from a
OY	1081 AAAGTAGCTGCTGAGCTTAAAGAAACTTGCACTTACGGTTAGTAA	1266	CC microorganism, where the antisense compound is complementary to GL or
Db	1261 GTTGTATGTTAAACAGGATCATGGCTTCAGAACAGGATTTAGCTGCA	1506	CC GS of a microorganism and specifically hybridises with and inhibits the
OY	1447 GTGATGATGATGTTAAACAGGATCATGGCTTCAGAACAGGATTTAGCTG	1386	CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral
Db	1260 1507 ATGCCAGCTCTGAGCTGAGCTTATTGACAAAGAGCACTTGCTAATAAC	1520	CC and antiproliferative activities, and can be used in antisense therapy
OY	1320 1507 ATGCCAGCTCTGAGCTGAGCTTATTGACAAAGAGCACTTGCTAATAAC	1520	CC for inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
Db	1321 1521 ATGCACTCTGAGCTGAGCTTATTGACAAAGAGCACTTGCTAATAAC	1380	CC also useful for inhibiting the growth of a microorganism or inhibiting
OY	1567 GACCAACTGCGACGCCAGCACTGAGCTTATTGACAAAGAGCACTTG	1625	CC the expression of GL or GS gene in a microorganism (a bacterial cell or
Db	1381 GAACCACTGCGCCAGGCCAGCATGCGAGGTTAGTGGGGG	1439	CC a virus) having a GL or GS gene which involves administering to the
RESULT 4			
ID	AAH56862 standard; DNA: 1306 BP.		CC microorganisms which involves identifying a eukaryotic organism
AC	AAH56862;		CC having a pathological condition mediated by microorganisms having a GL
XX			CC or GS gene and administering (I) such that the growth of microorganism
DT	05-SEP-2001 (first entry)		CC is inhibited. The antisense compounds are utilised for diagnostics
XX			CC and therapeutics, prophylaxis and as research reagents and kits, e.g., to
DE	Antibiotic resistant <i>S. pyogenes</i> groEL gene partial sequence SEQ ID:8.		CC prevent or delay microbial infections in humans. They are also useful as
XX			CC molecular weight markers. AAH56862 to AAH56367 and AAH56833 to AAH56854
DE	Antisense oligonucleotide; groE; groS; inhibitor; growth;		CC represent PCR primers for groE sequences which are used in the
XX			CC exemplification of the present invention. AAH56835 to AAH56870 represent
OS	Streptococcus pyogenes.		XX groE nucleotide sequence given in the present invention.
XX	WO200116625-A2.		SO Sequence 1306 BP; 407 A; 235 C; 308 G; 356 T; 0 other:
Query Match			
Best Local Similarity: 69.6%; Score: 110.4; DB: 22; Length: 1306;			
Matches: 1141; Conservancy: 99.9%; Pred. No: 1.9e-288; Mismatches: 1; Indels: 0; Gaps: 0;			
OY	484 GAGCTTGGCGGTGGCACGATGGTGGATTCATCGAGATCCTGGGTT	543	QY 484 GAGCTTGGCGGTGGCACGATGGTGGATTCATCGAGATCCTGGGTT
Db	2 GAAGCTTGGCGGTGGCACGATGGTGGATTCATCGAGATCCTGGGTT	61	Db 2 GAAGCTTGGCGGTGGCACGATGGTGGATTCATCGAGATCCTGGGTT
OY	544 GAACTGAGCTGAGTGGTGGAGGCATGCAATTGACGGGGTACTCTCTTCATAAC	603	QY 544 GAACTGAGCTGAGTGGTGGAGGCATGCAATTGACGGGGTACTCTCTTCATAAC
Db	62 GAAACAGACTGAGTGGTAAAGCATGCATGCAATTGACGGGGTACTCTCTTCATAAC	121	Db 62 GAAACAGACTGAGTGGTAAAGCATGCATGCAATTGACGGGGTACTCTCTTCATAAC
OY	604 ATGGCTACAGACGAAATGTTGAGACTGAAACCAATTACTTAAAG	663	QY 604 ATGGCTACAGACGAAATGTTGAGACTGAAACCAATTACTTAAAG
Db	122 ATGGCTACAGACGAAATGTTGAGACTGAAACCAATTACTTAAAG	181	Db 122 ATGGCTACAGACGAAATGTTGAGACTGAAACCAATTACTTAAAG
OY	664 GATAAAAGTCAACATCCAGACATTGCACTACTTGAGGAGTCCTAAAC	723	QY 664 GATAAAAGTCAACATCCAGACATTGCACTACTTGAGGAGTCCTAAAC
Db	182 GATAAAAGTCAACATCCAGACATTGCACTACTTGAGGAGTCCTAAAC	241	Db 182 GATAAAAGTCAACATCCAGACATTGCACTACTTGAGGAGTCCTAAAC
OY	724 AACGGTCCATTACTCATTTACAGATGATGTTGAGGAGCACTTCAACCTCTG	783	QY 724 AACGGTCCATTACTCATTTACAGATGATGTTGAGGAGCACTTCAACCTCTG
Db	242 AACGGTCCATTACTCATTTACAGATGATGTTGAGGAGCACTTCAACCTCTG	301	Db 242 AACGGTCCATTACTCATTTACAGATGATGTTGAGGAGCACTTCAACCTCTG
OY	784 TTGACACAGTTCTGGTCACTTCATGTTGCTGTTGCTGTTGCTGTTGCTG	843	QY 784 TTGACACAGTTCTGGTCACTTCATGTTGCTGTTGCTGTTGCTGTTGCTG
Db	302 TTGACACAGTTCTGGTCACTTCATGTTGCTGTTGCTGTTGCTGTTGCTG	903	Db 302 TTGACACAGTTCTGGTCACTTCATGTTGCTGTTGCTGTTGCTGTTGCTG
OY	844 CGCGTAACTGCTGAGACAGTCAGCTGTTGCTGTTGCTGTTGCTGTTGCTG	361	QY 844 CGCGTAACTGCTGAGACAGTCAGCTGTTGCTGTTGCTGTTGCTGTTGCTG
Db	362 CGTCGTAAGCTGCTGAGACAGTCAGCTGTTGCTGTTGCTGTTGCTGTTGCTG	421	Db 362 CGTCGTAAGCTGCTGAGACAGTCAGCTGTTGCTGTTGCTGTTGCTGTTGCTG

QY 904 GACTCTAGACTGTTGATTAAGATGACTCTACATGACNGCCCTTGACAGGCTGTCATAATT 963
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 422 GATCTCTAGACTGTTGATTAAGATGACTCTACATGACNGCCCTTGACAGGCTGTCATAATT 481
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 964 ACAGTTGATTAAGATGACAGTATGTTGAGGTTGAGGTTGAGGTTGAGGCTGAGGCTGTCATAATT 1023
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 482 ACAGTTGATTAAGATGACAGTATGTTGAGGTTGAGGTTGAGGCTGAGGCTGTCATAATT 541
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1024 ACCGGTTGACAGTAACTCAATTAGAACACACTCTGACTTGACGGTCAAGCTTGACGGTGA 1083
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 542 ACCGGTTGACAGTAACTCAATTAGAACACACTCTGACTTGACGGTCAAGCTTGACGGTGA 601
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1084 AACTACAGAAGACCTTGGCAAAATCTGCTGTTGAGCTGCTGTTATCAAGAATGAGGCT 1143
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 602 AACTACAGAAGACCTTGGCAAAATCTGCTGTTGAGCTGCTGTTATCAAGAATGAGGCT 661
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1144 CCAACAGAGACGCTTAAAGAATGAACTCOCATGAGATCTGAGATCTTAATGTACA 1203
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 662 CCAACAGAGACGCTTAAAGAATGAACTCOCATGAGATCTGAGATCTTAATGTACA 721
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1204 CTCGAGCCCTTGGAGGTTGCTGCTGCTGGACAGCACTTTAGGTT 1263
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 722 CGTGACGCCCTTGGAGGTTGCTGCTGCTGCTGGACAGCACTTTAGGTT 781
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1264 GAAAGAGTGAACGCTTGGAGGTTAATGAACTCOCATGAGATCTGAGATCTTAATGTACA 1323
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 782 GAAAGAGTGAACGCTTGGAGGTTAATGAACTCOCATGAGATCTGAGATCTTAATGTACA 1323
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1324 CGTGCTCTAGAACGCTGACGCTGAACTGCTTAAATGCGGTACAGCTGCCGA 1383
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 842 CGTGCTCTAGAACGCTGACGCTGAACTGCTTAAATGCGGTACAGCTGCCGA 901
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1384 GTTATGACAGTGTGAAACACGCCNGCAGAACGAGTTAATGCTGCAACAGTGG 1443
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 902 GTTATGACAGTGTGAAACACCCCTGAGAACGAGTTAATGCTGCAACAGTGG 961
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1444 TGGGTGATGATGTTAAACAGGAACTGACGCTGTCAGTAAACGATGACGCTT 1503
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 962 TGGGTGATGATGTTAAACAGGAACTGACGCTGTCAGTAAACGATGACGCTT 1021
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1504 CAAATGACGCTCTGTTGACGAGCCTGCTGCTTAAAC 1563
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1022 CAAATGACGCTCTGTTGACGAGCCTGCTGCTTAAAC 1081
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1564 CCTGACCAAGCTTCAACCGCCAGCATGCCACGCTGTTGAGTGTGCTTAAAC 1623
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1082 CCTGACCAAGCTTCAACCGCCAGCATGCCACGCTGTTGAGTGTGCTTAAAC 1141
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 1624 GG 1625
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1142 GG 1143
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 5
 AAH5685 AAH5686 standard; DNA; 1305 BP.

AC AAH5686;
 XX 06-SEP-2001 (first entry)

XX Antibiotic resistant *S. pyogenes* groEL gene partial sequence SEQ ID:11.

XX Antisense oligonucleotide; groEL; groES; inhibitor; growth;
 XX microorganism; *Escherichia coli*; *Streptococcus pneumoniae*;
 XX *Streptococcus* progenes; *Staphylococcus aureus*; *Pseudomonas aeruginosa*;
 XX antibacterial; antibiotic; antiproliferative; antisense therapy;
 XX microbial infection; ds.

OS Streptococcus Progenes.

XX WO200136625-A2.

QY 689 TATGGACCCGTGGCCACAGATGGTGTACATCGAGAACATCGAGGTTGAGAAC 548
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 TATGGACCCGTGGCCACAGATGGTGTACATCGAGAACATCGAGGTTGAGAAC 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 549 AGACTTGAGTGTCAACGCACTGCAATTGACCGTGTACCTCTCAATCTGGT 608
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 61 AGACTTGAGTGTCAACGCACTGCAATTGACCGTGTACCTCTCAATCTGGT 608
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 609 CACAGCAATGAAATGTTGAGCTTACATGTTAATGCGATA 668
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 121 CACAGCAATGAAATGTTGAGCTTACATGTTAATGCGATA 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 669 AAAGTGTCAACGCACTGCAATTGACCGTGTACCTCTCAATCTGGT 728
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 181 AAAGTGTCAACGCACTGCAATTGACCGTGTACCTCTCAATCTGGT 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 729 TCCATTAATGCACTGAGTGTGAGTGTGAGCTTACCCCTGCTGAAACCTGTC 788
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 241 TCCATTAATGCACTGAGTGTGAGTGTGAGCTTACCCCTGCTGAAACCTGTC 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Query Match 68.5%; Score 1122.6; DB 22; Length 1305;
 Best Local Similarity 99.2%; Pred. No. 8.7e-284;
 Matches 1128; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 SQ Sequence 1305 bp; 406 A; 238 C; 312 G; 349 T; 0 other;

OY	789	CAAGATTCGGGACATCAATGGGTTGTCGAAACGCCAGGGATGGATGTCG	848	PN	WO200234771A2.
Db	301	CAAGATTCGGGACATCAATGGGTTGTCGAAACGCCAGGGATGGATGTCG	360	PD	02-MAY-2002.
OY	849	TAACCTATGCTGAGACATTCCTACTTGACCGGGGTCAGCTATCAGAGACT	908	XX	
Db	361	TAACCTATGCTGAGACATTCCTACTTGACCGGGGTCAGCTATCAGAGACT	420	PF	29-OCT-2001; 2001WO-GB04789.
OY	909	ARGACITGATTAAGATGCTCAATGACAGCCCTGGACAGCTGAGATACGT	968	XX	
Db	421	ARGACITGATTAAGATGCTCAATGACAGCCCTGGACAGCTGAGATACGT	480	PR	27-OCT-2000; 2000GB-0026333.
OY	969	TGATTAAGATGACAGCTAATGGAGGTGAGCTAACATGACAGCCCTGGAC	1028	PR	07-MAR-2001; 2001GB-0005640.
Db	481	TGATTAAGATGACAGCTAATGGAGGTGAGCTAACATGACAGCCCTGGAC	540	XX	(CHIR-) CHIRON SPA.
OY	1029	TATGCCACGATTAATGCCATTAGAACACACTTGACTTGACCTGAAACT	1088	PA	(GENO-) INST GENOMIC RES.
Db	541	TATGCCACGATTAATGCCATTAGAACACACTTGACTTGACCTGAAACT	600	XX	
OY	1089	ACAGAGAAGTGGGGAATTAGCTGTTGCTGTTGAGCTGTTGAGGTTCC	1148	PT	New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
Db	601	ACAGAGAAGTGGGGAATTAGCTGTTGCTGTTGAGCTGTTGAGGTTCC	660	PT	for detecting a compound that binds to the protein -
OY	1149	AGAGACAGCTTGGCCTAAAGATGAACTTCCATGAGCTGTTGAGGTTCC	1208	XX	Claim 7; Page 3785; 4525pp; English.
Db	661	AGAGACAGCTTGGCCTAAAGATGAACTTCCATGAGCTGTTGAGGTTCC	720	CC	The invention relates to a protein (ABP25413-ABP30895) from group B Streptococcus/BS (Streptococcus agalactiae), given in the specification. The proteins have antibacterial and anti-inflammatory activity. (1), nucleic acids encoding (1), ABN6044-ABN71326 and (Streptococcus pyogenes), comprising one of 543 sequences (S1), given in (2).
OY	1209	ACGCTTGAGGAGTGGTGTCTGTTGAGCTGTTGAGGTTCC	1268	CC	CC
Db	721	ACGCTTGAGGAGTGGTGTCTGTTGAGCTGTTGAGGTTCC	780	CC	CC
OY	1269	AGTACACTCTGACTTGAGGCGATGAGCTACTGGAGCTTAACTGTC	1328	CC	CC
Db	781	AGTACACTCTGACTTGAGGCGATGAGCTACTGGAGCTTAACTGTC	840	CC	CC
OY	1329	TCTAGAAGAGCTGACCTCAATTGCTTAATGGGTTGACGAGCCGTT	1388	CC	CC
Db	841	TCTAGAAGAGCTGACCTCAATTGCTTAATGGGTTGACGAGCCGTT	900	CC	CC
OY	1389	TGACAGTTGAAACAGGCCCTGCGAGCAGATTAACTGTCACAGTG	1448	CC	CC
Db	901	TGACAGTTGAAACAGGCCCTGCGAGCAGATTAACTGTCACAGTG	960	CC	CC
OY	1449	TGATATGATTAAACAGGATATGACCTGTCAGTACAGTCAGCTCAA	1508	CC	CC
Db	961	TGATATGATTAAACAGGATATGACCTGTCAGTACAGTCAGCTCAA	1020	CC	CC
OY	1509	TGCACTCTTGACTCTTTGACACAGGATGTCGAAAGTACAGTCAGCT	1568	CC	CC
Db	1021	TGCACTCTTGACTCTTTGACACAGGATGTCGAAAGTACAGTCAGCT	1080	CC	CC
OY	1569	ACCAGCTAGGCCAGGCCAGCATGCCAGCAGTTGATCCAGATGTTG	1625	CC	CC
Db	1081	ACCAGCTAGGCCAGGCCAGCATGCCAGCAGTTGATCCAGATGTTG	1137	CC	CC
RESULT 6					
ID	ABN69159	standard; DNA; 1620 BP.		SQ	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
AC	ABN69159;			Query Match	54.9%; Score 1062.4; DB 24; Length 1620;
XX				Best Local Similarity	79.8%; Pred. No. 5.5e-268;
XX				Matches	1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX				CC	79.8%; Pred. No. 5.5e-268;
XX				CC	Matches 1274; Conservative 0; Mismatches 331; Indels 1;
XX				CC	Sequence 1620 BP; 498 A; 271 C; 390 G; 461 T; 0 other;
XX				CC	Query Match
XX				CC	54.9%; Score 1062.4; DB 24; Length 1620;
XX				CC	Best Local Similarity
XX					

QY	361	ACGCAACAGCAACAGCTGTTGAGACCTGAAAGCACTGTCACCTGTATGGCAG 420	DB	1441	GAATGGTAGATATGGTTACACAGGTTACAGTCAGTCAAGTACAGTCTGCA 1500
Db	361	ACAGCTTGTGTCAGCACTGAGCTTGTGAGGAGCTAAAGAGATCACACCGTTGGAA 420	QY	421	GAAGCTATGCTCAGGCGCTGCACTATCATGACGCTCTGAAAGAAAGTTGGAGATATC 480
Db	421	GAAGCTATGCTCAGGCGCTGCACTATCATGACGCTCTGAAAGAAAGTTGGAGATATC 480	DB	421	GAAGCTATGCTCAGGCGCTGCACTATCATGACGCTCTGAAAGAAAGTTGGAGATATC 480
QY	481	TCTGAGCTATGGCGCGTGGTGTGATATGCTGTTGAGTATGGCTCTGAAAGAAAGTTGGAGATATC 540	QY	481	TCTGAGCTATGGCGCGTGGTGTGATATGCTGTTGAGTATGGCTCTGAAAGAAAGTTGGAGATATC 540
Db	481	TCTGAGCTATGGCGCGTGGTGTGATATGCTGTTGAGTATGGCTCTGAAAGAAAGTTGGAGATATC 540	DB	481	TCTGAGCTATGGCGCGTGGTGTGATATGCTGTTGAGTATGGCTCTGAAAGAAAGTTGGAGATATC 540
QY	541	ATGGAAACAGACTGTGAGTTGAGGCTGATTTGACCGGTTTACCTGTCAC 600	QY	541	ATGGAAACAGACTGTGAGTTGAGGCTGATTTGACCGGTTTACCTGTCAC 600
Db	541	ATGGAAACAGACTGTGAGTTGAGGCTGATTTGACCGGTTTACCTGTCAC 600	DB	541	ATGGAAACAGACTGTGAGTTGAGGCTGATTTGACCGGTTTACCTGTCAC 600
QY	601	TACATGGTCAGAGACAATGAAAGAAATGTTGACGCTTGAAACCAATTATC 660	QY	601	TACATGGTCAGAGACAATGAAAGAAATGTTGACGCTTGAAACCAATTATC 660
Db	601	TACATGGTCAGAGACAATGAAAGAAATGTTGACGCTTGAAACCAATTATC 660	DB	601	TACATGGTCAGAGACAATGAAAGAAATGTTGACGCTTGAAACCAATTATC 660
QY	661	ACGATTAAGAAAGTCACACATCCAAAGACATTGCACTCTTGAGGAGTCCTAA 720	QY	661	ACGATTAAGAAAGTCACACATCCAAAGACATTGCACTCTTGAGGAGTCCTAA 720
Db	661	ACGATTAAGAAAGTCACACATCCAAAGACATTGCACTCTTGAGGAGTCCTAA 720	DB	661	ACGATTAAGAAAGTCACACATCCAAAGACATTGCACTCTTGAGGAGTCCTAA 720
QY	721	ACGACCGCCGCACTTACATCAATTGCAAGAAATTCAGCTTACATTC 780	QY	721	ACGACCGCCGCACTTACATCAATTGCAAGAAATTCAGCTTACATTC 780
Db	721	ACGACCGCCGCACTTACATCAATTGCAAGAAATTCAGCTTACATTC 780	DB	721	ACGACCGCCGCACTTACATCAATTGCAAGAAATTCAGCTTACATTC 780
QY	781	GCCTGAAAGAAAGTTGTTGTTAATTCAGTGTGTTGCAAGGCCAGATTTG 780	QY	781	GCCTGAAAGAAAGTTGTTGTTAATTCAGTGTGTTGCAAGGCCAGATTTG 780
Db	781	GCCTGAAAGAAAGTTGTTGTTAATTCAGTGTGTTGCAAGGCCAGATTTG 780	DB	781	GCCTGAAAGAAAGTTGTTGTTAATTCAGTGTGTTGCAAGGCCAGATTTG 780
QY	841	GATCGCTGTAAGCTATGCTGTTGACGATTCATCTTGACGGGTTGACGGGT 900	QY	841	GATCGCTGTAAGCTATGCTGTTGACGATTCATCTTGACGGGTTGACGGGT 900
Db	841	GATCGCTGTAAGCTATGCTGTTGACGATTCATCTTGACGGGTTGACGGGT 900	DB	841	GATCGCTGTAAGCTATGCTGTTGACGATTCATCTTGACGGGTTGACGGGT 900
QY	901	GAGGATCTGAGCTGTGTTAAGATGCTCTAATGAGCCTTGAGACGGCTGTG 960	QY	901	GAGGATCTGAGCTGTGTTAAGATGCTCTAATGAGCCTTGAGACGGCTGTG 960
Db	901	GAGGATCTGAGCTGTGTTAAGATGCTCTAATGAGCCTTGAGACGGCTGTG 960	DB	901	GAGGATCTGAGCTGTGTTAAGATGCTCTAATGAGCCTTGAGACGGCTGTG 960
QY	961	ATTCAGTGTGAAAGATGAGCTGAGCTGAGTGTGAGGAGTCAGCTT 1020	QY	961	ATTCAGTGTGAAAGATGAGCTGAGCTGAGTGTGAGGAGTCAGCTT 1020
Db	961	ATTCAGTGTGAAAGATGAGCTGAGTGTGAGGAGTCAGCTT 1020	DB	961	ATTCAGTGTGAAAGATGAGCTGAGTGTGAGGAGTCAGCTT 1020
QY	1021	GCTAACCGTTATGCTGATTTGAACTTACATCAATTGCAACACTCTGACTT 1080	QY	1021	GCTAACCGTTATGCTGATTTGAACTTACATCAATTGCAACACTCTGACTT 1080
Db	1021	GCTAACCGTTATGCTGATTTGAACTTACATCAATTGCAACACTCTGACTT 1080	DB	1021	GCTAACCGTTATGCTGATTTGAACTTACATCAATTGCAACACTCTGACTT 1080
QY	1141	GCTCTCAACAGACACCTTAAGAAAGATGAACTGCTGCTAATGCT 1200	QY	1141	GCTCTCAACAGACACCTTAAGAAAGATGAACTGCTGCTAATGCT 1200
Db	1141	GCTCTCAACAGACACCTTAAGAAAGATGAACTGCTGCTAATGCT 1200	DB	1141	GCTCTCAACAGACACCTTAAGAAAGATGAACTGCTGCTAATGCT 1200
QY	1201	ACAGCTGCTGAGCTGTGAGAAAGCTATGCTGCTGCTGAGACAGCTATTAAGGT 1260	QY	1201	ACAGCTGCTGAGCTGTGAGAAAGCTATGCTGCTGCTGAGACAGCTATTAAGGT 1260
Db	1201	ACAGCTGCTGAGCTGTGAGAAAGCTATGCTGCTGCTGAGACAGCTATTAAGGT 1260	DB	1201	ACAGCTGCTGAGCTGTGAGAAAGCTATGCTGCTGCTGAGACAGCTATTAAGGT 1260
QY	1261	ATTGAAAGATGCGAGCTTGTGAGGGGGAGATGCTACTGGCTAACATG 1320	QY	1261	ATTGAAAGATGCGAGCTTGTGAGGGGGAGATGCTACTGGCTAACATG 1320
Db	1261	ATTGAAAGATGCGAGCTTGTGAGGGGGAGATGCTACTGGCTAACATG 1320	DB	1261	ATTGAAAGATGCGAGCTTGTGAGGGGGAGATGCTACTGGCTAACATG 1320
QY	1321	CTTGGTGTCTGAGAGACGCTGTGACTCAATTTGCTTAATGCTGTTGAGGCGCT 1380	QY	1321	CTTGGTGTCTGAGAGACGCTGTGACTCAATTTGCTTAATGCTGTTGAGGCGCT 1380
Db	1321	CTTGGTGTCTGAGAGACGCTGTGACTCAATTTGCTTAATGCTGTTGAGGCGCT 1380	DB	1321	CTTGGTGTCTGAGAGACGCTGTGACTCAATTTGCTTAATGCTGTTGAGGCGCT 1380
QY	1381	CTTGGTGTCTGAGAGACGCTGTGACTCAATTTGCTTAATGCTGTTGAGGCGCT 1440	QY	1381	CTTGGTGTCTGAGAGACGCTGTGACTCAATTTGCTTAATGCTGTTGAGGCGCT 1440
Db	1381	CTTGGTGTCTGAGAGACGCTGTGACTCAATTTGCTTAATGCTGTTGAGGCGCT 1440	DB	1381	CTTGGTGTCTGAGAGACGCTGTGACTCAATTTGCTTAATGCTGTTGAGGCGCT 1440
QY	1441	GACGGGGTGTGATTAACAGGAATCATGGACCTGTGCAAGTACAGATCAGCG 1500	QY	1441	GACGGGGTGTGATTAACAGGAATCATGGACCTGTGCAAGTACAGATCAGCG 1500

Best Local Similarity	79.2%	Pred.	No. 9.8e-267;	Nucleic acids encoding conserved essential genes involved in bacterial
Nucleotides	1244;	Conservative	0;	reputation which are potential targets for the treatment of antibiotic
Matches	331;	Mismatches	3;	resistance.
Indels	3;	Gaps	1;	Resistance to antibiotics is a major concern in medicine and
Db	2023129	GCTAACGCGTAGCTATCATTAAGTCACNGATGGAGGCTACACTCTGATTGATCGT	2023190	antibiotic resistance. One of the most common mechanisms of
Qy	1081	GAAACATCAAGAAGGTGGGAATTAGCTGTTGGTGTAGTGTATGAGTAGA	1140	resistance is the production of enzymes that inactivate the antibiotic.
Db	2023189	GAAATTACAGACGACTTGCTAAGTGCAGCTAATGCGGTTGAGT	2023130	For example, beta-lactamases are enzymes that can hydrolyze the
Qy	1141	GCTCAAGAGACAGCTTAAAGAAGTCAACTCGCATGGATGCTTAATGCT	1200	beta-lactam ring of penicillin and cephalosporin antibiotics.
Db	2023129	GCACGACTGAAAGAATTAAGAGTAAACTGCTAACAGTTCATGTTAATGCA	2023070	Other mechanisms include the modification of the antibiotic target
Qy	1201	ACAGTGACGGTGTGAGAAGTGTACCTGCGGACTAATGTTGTCAGAGTGC	1240	site or the production of efflux pumps that can transport the antibiotic
Db	2023069	ACGGTCTGAGGTTGACAGGTTGAGGTTGAGGTTGAGGACTATTACGGT	1260	out of the cell.
Qy	1261	CITCGCTCTAGAGAGCCGTGAGCTTAAATGCTGAGGCTTCAGCTTCG	1380	Antibiotic resistance is a complex problem that requires a multi-faceted
Db	202309	ATGAAAAATAGGGCTGAGCTTAAACAGCTGTTGAGGTTGAGGTTCA	2023090	approach to address. This includes the development of new antibiotics,
Qy	1381	GTACGTTAGCAGCTTAAACAGCTGTTAATGCTGAGGTTGAGGTTCA	2022890	the discovery of new resistance inhibitors, and the improvement of existing
Db	2022889	GTATTATTGACGTTAAACAGCTGTTAATGCTGAGGTTGAGGTTATGGCAGATG	2022830	therapies.
Qy	1441	GAGGGGTGATGATTAACAGAACTGACGGCTCAAGAACGCTGAGGTTATGCTG	1500	Overall, the study of antibiotic resistance is crucial for the development of
Db	2022829	GATGGTATATGGTACACAGTATGACCGTATGACCGCTTCAGCA	2022770	new treatments and the prevention of antibiotic resistance.
Qy	1501	CTTCAAAATGACGCTCTGCTACTGCTTATTTTACACACAAAGCTGAGT	1560	Yours sincerely,
Db	2022769	CTTCACAAATTCGGCATGTCAGCTTCTGCACTTCTGACGACTGAGCTG	2022710	John Doe
Qy	1561	AGCTACGCCAGGCGAGAACTCAGCAGCTTCTGAGCTTCTGACGACTGAGCTG	1605	Yours sincerely,
Db	2022709	AAACTGACCAAGCTCTACAGCTCTGCAATGATCCATCTATG	2022662	John Doe
RESULT	8			
AAH90800				
ID	AAH90800	standard; DNA; 1623 bp.		
AC	AAH90800;			
DT	02-OCT-2001 (first entry)			
DE	CPE 104 coding sequence.			
XX				
KW	Antibacterial; vaccine; gene therapy; bacterial cell wall viability;			
KW	CPE; CEG; Conserved Essential Gene; bacterial infection;			
KW	antisense therapy; antibiotic resistance; ds.			
OS	Streptococcus pneumoniae.			
XX				
PN	W0200149721-A2.			
PD	12-JUL-2001.			
XX				
PR	29-DEC-2000; 2000040-0535604.			
XX				
PR	30-DEC-1999; 9905-0174089.			
XX				
PA	(BRIM) BRISTOL-MERS SQUIBB CO.			
XX				
PI	Dougherty T.J., Pucci MJ, Dougherty BA, Davison DB, Bruccoleri RE;			
PI	Thanassi JA;			
XX				
DR	WPI: 2001-96721/54.			
DR	P-PSDB; AAM0101.			
PT	Nucleic acids encoding conserved essential genes involved in bacterial			
PT	reputation which are potential targets for the treatment of antibiotic			

PT
resistant bacterial infections -XX
PS
Claim 16, Page 231; 380pp; English.

XX
The present invention relates to nucleic acids (A9H90701-A9H90918) encoding polypeptides (AM01002-AM0111), which are essential for the viability of a bacterial cell wall. The acronym CEG stands for "CEG Expression", where CEG stands for "Conserved Essential Gene". The nucleic acids are useful for detecting the presence of proteins essential for the viability of a bacterial cell wall in samples such as cells, tissues, biological fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleotide sequence of interest is essential for viability of a bacterial cell or whether it resides within an operon by integrating an exogenous nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest (comprising 200-500 base pairs) into the genomic sequence of interest which confers a selectable phenotype to the cell, and determining cell viability with a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids also enable identification of targets suitable for the treatment of antibiotic resistant bacterial infections.

XX
Sequence 1623; BP: 490 A; 325 C; 394 G; 414 T; 0 other:

Query Match 63.4%; Score 1039.2; DB 22; Length 1623;
Best Local Similarity 77.8%; Pred. No. 6.6-262;
Matches 1257; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

QY 1 ATGGCAGAAAGAAGAAATCAAAATTCTCGAGATCGGGCTGCGGAGATGAT 60
Db 1 ATGGCAGAAAGAAGAAATCAAAATTCTCGAGATCGGGCTGCGGAGATGAT 60
QY 61 ATGGTAGAGATACCGCGAACAGTACCTGAGCTTGCTCTAAAGGGCGAATG 120
Db 61 ATTCCTGCAAGCTGTTAGATGACCTGGACCAAAGGTGCAAGCTGCTTGA 120
QY 121 AATGGTTATGCTCGCGTAATACATAGACGGGAACATTGTCGAGTGGCTAA 180
Db 121 ATGGTAGATGGTTACCGCTGATACCGTGGACATGGACATGGCAAGAATG 180
QY 181 TTAGAGACGATTGAAACATGGGGCAAAATTGGTCTGAGTGGCTCTAAACC 240
Db 181 TTAGAGACGATTGAAACATGGGGCAAAATTGGTCTGAGTGGCTCTAAACC 240
QY 241 ATGGATATGCTGGTGTGATGGGACGACTGCAACATTGACGACAGCTTCA 300
Db 241 ATGGATATGCTGGTGTGATGGGACGACTGCAACATTGACGACAGCTTCA 300
QY 301 GAAAGCACTAAATGATGACGAGCGATGCTAAATCCATTGTTGCGGAGGATTA 360
Db 301 GAAAGCACTAAATGATGACGAGCGATGCTAAATCCATTGTTGCGGAGGATTA 360
QY 361 ACAGGAAACGCAACACTGTGACGACGCTTAAAGCCATGCTGCACTCGCGA 420
Db 361 ACAGCAGTGGCGGACGACTGTGAGCTTGAACAAACACGCACTCCCGTGC 420
QY 421 GAACTGATGCTGGCTGGGATGCTGAGATGCTGAGATGCTGAGATGCTGAGT 480
Db 421 GAACTGATGCTGGCTGGGATGCTGAGATGCTGAGATGCTGAGATGCTGAGT 480
QY 481 TCACTGGTCACAGACATGAAATAATGGTGCAGCTGAACTTATGCTGAGT 540
Db 481 TCTGGAGGAACTGAAAGTGCCAAAGGGCTGCTACATGAGACTTCAGCTG 540
QY 541 ATGGAAACGAACTGAACTGGTGTGAGGCATGCAATTGACCTGGTGTGCTAA 600
Db 541 ATGGAAACGAGCTGAACTGGTGTGAGGAGTGGCTGACCTGGTGTGCTAA 600
QY 601 TCACTGGTCACAGACATGAAATAATGGTGCAGCTGAACTTATGCTGAGT 660
Db 601 TACATGGTGACAGATAGCCAAAAATGGTGTGCTGAGCTTGAATTCGGTACATTTGATT 660

Db 661 ACGGATAAAAGTCACACATCCAGACATTGCACTACTTGAGGAGTCTTAA 720
Db 661 ACAGACAGAAATTCACACATCCAGACATTGCACTACTTGAGGAGTCTTAA 720
QY 721 ACCAACCTCCATTACTCATATTGCGAGATGAGTGTGAGCTTGGAAACCTT 780
Db 721 ACCACCTCCACTCTGTGTTATGGGATGATGTTGGAGTGGAGCTTCACCTT 780
QY 781 GCTGTAACAGATCTGTGTTCTGATGCTGCTTCAAGGGCAAGGATTGGT 840
Db 781 GTTGTGACAGATGCGAGCTTCAAGGGCAAGGATTGGT 840
QY 841 GATGCTCTTAAGCTATGGTGTGAGACATGCTATCTGACGAGTGTGCTACATCA 900
Db 841 GACCTCGAACGATCTGTGTTATGGAGATGCGCTTAAAGCTGAGTACACA 900
QY 901 GAGATCCAGACTGTAATGAAAGTGTACATGAGTGTGAGTGTGAGTGTGAGT 960
Db 901 GAGACCTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 960
QY 961 ATTCACTGTGATAAGATGACGACATTAATGTTGAGGTTGAGGTTGAGGTTGAGGATT 1020
Db 961 GTGACCGGGACAAAGATGACGCTTGTGAGGGTGTGAGGAAATCTGGCGTAC 1020
QY 1021 GCTAACCTATGCACTGATTAATGCAATTGAAACACAACTCTGACTTGACCT 1080
Db 1021 TCTCACCGTGTGGCTTATCAGTCATGCAACTACACTCTGTGATTTGACCT 1080
QY 1081 GAAACACTAACAGACGCTTGGCAAAATAGCTGGGTTGCTGTATCAAGTGA 1140
Db 1081 GAAATATGTCAGAACAGCTTGGCCAATATGCTGGGTTGCTGTATCAAGTGA 1140
QY 1141 GCTCCACAGAGACAGCTTAAGAAATGAACTTCGATGTTGAGTCTCTAATGCT 1200
Db 1141 GCGGCACTGAACTGAGTGTGAAKAGTGGACATTCGGCATTTGAGTGCCTCAACGCT 1200
QY 1201 ACAGCTGACGCGTGTGAGAAGTGTCTGTTGTTGGGGGGGAGACACTTAA 1260
Db 1201 ACTCGTGCAGCTGTGAGAAGTGTCTGTTGAGTGTCTGTTGGGGGGGAGACACTCTGGCAATGTG 1260
QY 1261 ATGGAAAGAATGAGCTTGAGCTGAGGAGTGTCTGTTGGGGGGGAGACACTTAA 1320
Db 1261 ATTCGACTGTGTTCTCTTGAACTGAGCAGAGTGTCTGTTGGGGGGGAGACACTTAA 1320
QY 1321 CTGGCTCTAGAGGCCCTGAGTGTAAATGCTTAAAGCTGGTGTGAGGCTCC 1380
Db 1321 CTGGCTCTAGAGGCCCTGAGTGTAAATGCTTAAAGCTGGTGTGAGGCTCC 1380
QY 1381 GATGTTATGACGAGTGTGAAACAGCCCTGAGGACAGGTTATGCTGAGGT 1440
Db 1381 ATGGATATGCACTCTTGTGAAATCTGAGTGTGAGGTACACCGACACTGGC 1440
QY 1441 GATGTTATGATGAAACAGGAGTGTGAGGCTGAGTGTGAGGTATGCTGAGGT 1500
Db 1441 GATGTTATGATGAGTGTGAGGCTGAGGTTATGCTGAGGTATGCTGAGGT 1500
QY 1501 CTTCAAATACGATCTGAGTGTGAGTGTGAGGTATGCTGAGGTATGCTGAGGT 1560
Db 1501 CTACAAATACGATCTGAGTGTGAGTGTGAGGTATGCTGAGGTATGCTGAGGT 1560
QY 1561 AACCTGACGAGCTAGGCGAGCGCAGCAATGCGAGGAGTGTGAGGTATGCTGAGGT 1620
Db 1561 AACACGAGACGAGCTAGGCGAGCGCAGCAATGCGAGGAGTGTGAGGTATGCTGAGGT 1620
Db 1561 AACACGAGACGAGCTAGGCGAGCGCAGCAATGCGAGGAGTGTGAGGTATGCTGAGGT 1620
RESULT 9
AAFP25036
ID AAF25036 standard; DNA; 1926 BP.
XX
AAFP25036;

DT 30-APR-2001 (first entry)

XX DE Nucleotide sequence of Hsp65-E7 fusion protein.

XX KW Heat shock protein; Hsp⁷; Th1 response; Th1 cell; CD4+ T lymphocyte cell; KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen; E7 protein; ss.

XX OS Synthetic.

OS Streptococcus pneumoniae.

XX Human papillomavirus.

Key CDS

FT Location/Qualifiers

FT 1..1926 /product= "Hsp65-E7 fusion protein"

FT XX w0200104344-A2.

FT XX 18-JAN-2001.

FT XX 10-JUL-2000; 2000W0-US18828.

PR XX 08-JUL-1999; 99US-0143757.

PA XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

PI XX Siegel, M., Chu NR., Mizzen LA;

DR XX WPI; 2001-138361/14.

DR XX P-PSDB; AAB31619.

PT Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells

PS XX Example 15; FIG 15A-B; 88pp; English.

XX The present sequence encodes a fusion protein comprising a Streptococcus pneumoniae heat shock protein (Hsp) 65 fused to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naïve lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the Th1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial pathogens.

XX Sequence 1926 BP; 585 A; 382 C; 464 G; 495 T; 0 other;

Query Match 63.4%; Score 1038.4; DB 22; Length 1926; Best Local Similarity 77.5%; Pred. No. 1.1e-261; Matches 1258; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

DB 241 AATGATATGCCAGGTGGAGCTACACTGCAACTGTTGACCCAAAGCAACGGCGT 300

QY 301 GAAGGCTAAATGCGACAGCGTGTCAATCCAAATGATGATCGTGGAGCATGAA 360

DB 301 GAAGGATCAACAGTACAGCGTGTCAATCCAAATGATGATCGTGGAGCATGAA 360

QY 361 ACGACACAGCAAGCTGTTGAGCCUTGAAAGCATTGCAACCTGCAACTGCTGTGGCAAG 420

DB 361 ACGACAGTGGCGGAGGAGTGAAGCTTGTGAAACACAGTATCCCTGTTGCCATRAA 420

QY 421 GAAGCTTGTCTCAGTGTGAGCGCTATCTCTCTGTCAGTGGAGGTATATC 480

DB 421 GAAGCTTGTCTCAGTGTGAGCGCTATCTCTCTGTCAGTGGAGGTATATC 480

QY 481 TCGAAGCTTGGAGCTGTGGACCATGTTGATTCACATCGAAGATATCCTCGAGT 540

DB 481 TCTGAAGCAATGGAAAGTGGCAAGACGCTGTCACCATGTCAGTGGAGCTGGT 540

QY 541 ATGGAACAGAACTGAGTGTGAGGAACTGCTGAAAGTGGTGAAGGCCTGCA 600

DB 541 ATGGAACAGAACTGAGTGTGAGGAACTGCTGAAAGTGGTGAAGGCCTGCA 600

DB 601 TACATGTTGACAGATGGAAAGTGGTGAAGACGCTGTCAGTGGAGCTGGT 660

DB 601 TACATGTTGACAGATGGAAAGTGGTGAAGACGCTGTCAGTGGAGCTGGT 660

QY 661 AGGATAAAACTGCAACATCGAACAGACATTGCAACTTGCACACTTGAGGA 720

DB 661 AGGAGAGAAATTCCATATCCAGAAGAACTCTGCAACCTT 720

QY 721 ACCAACGGTCAATTCTATGCAAGATGCTGAGCTTGTGAACTTCACCC 780

DB 721 AGCAATGCCACTCTGTATATGGGAGATTTGGAGACGATTCACCC 720

QY 781 GCTGAGAAAGTGGTGTACTTCATGTTGATGCTGCAAGCSCCAGATTGG 840

DB 781 GTTTGGACAAAGTGGTGTAACTTCACAGTGGTGTACTTCAC 840

QY 841 GATGGCCTGAACATGCTGAGACATGCTGAGATGCTGTTGAGGAGGT 840

DB 841 GACCGGCGAAAGCCATGCTGAGATGCTGTTGAGGAGGT 840

DB 900 GAGGACTGGTGTGAGTGAAGTAAAGATGCCACATGACASCCCTGGACAGGGCTCTAG 960

DB 901 GAGGACTGGTGTGAGTGAAGTAAAGATGCCACATGACAGGGCTCTAG 960

QY 961 ATTACAGTGTATGATGACAGATGACATGTTGAGGTGAGTCAAGAACCT 1020

DB 961 GGGACCGTGGACAAAGATGACAGGGTATGGAGGGAAATCTGAGGGAT 1020

QY 1021 GCTAACCTGTTGACTGTAAATGCAATTGAGAACACAACTTCGACTTGACCT 1080

DB 1021 TCTCACCCCTGCGCTTATCAGTGTCAATGAACTACAACTTCGACTTGACCT 1080

QY 1081 GAAAATCAAGAACGTTGGGAATATGCTGTTGAGCTGTATCAATGAA 1140

DB 1081 GAAAATTCAGAACGCTGCAATGCTGAGCTGTGTTGAGCTGTATCAATGAA 1140

QY 1141 GCTCAACAGACAGCTTAAAGAAACTGCACTGCTGTGAGATGCTTAATGCT 1200

DB 1141 GCGCAACTGAACTGAGTGTGAGAAATGCAACTCGCTGTGAGATGCTTAATGCT 1200

DB 1201 ACTGGCTGAGCTGTGAGAAGTGTGAGCTGTGAGGAGCTGTCAGTGTG 1260

QY 1261 ATTGAAAGTGTGAGCTGTGAGCTGTGAGGAGCTGAGTCACTGCAACATGTC 1320

DB 1261 ATTCAGCTGTCACCTGTGAGCTGTGAGGAGCTGAGTCAACAGGACATGTC 1320

QY 1321 CTTGGTGTCTAGAGAGSCTTACCTCAATGCTTAAATCTGGTGTGAGGCTCC 1380

QY	541	ATGGAAACAGACAGACTTGAGTGGTGAAGSGCAGATTGACGGTGTACCTGCTCAA	600	RESULT 12
Db	541	ATGGAAACAGACAGACTTGAGTGGTGAAGSGCAGATTGACGGTGTACCTGCTCAA	600	AH56860
QY	601	TACATGTCAGACGACGAAATGGTGGAGCTTGACCTGAAACCATTTATTCATC	660	ID AH56860 standard; DNA: 2107 BP.
Db	601	TACATGTCAGACGACGAAATGGTGGAGCTTGACCTGAAACCATTTATTCATC	660	XX
Db	601	TACATGTCAGACGACGAAATGGTGGAGCTTGACCTGAAACCATTTATTCATC	660	AC
QY	661	ACGGATAAAAGTGTCAAGCAAGCAAGCATCTTGAGGAGTCAA	720	AH56860;
Db	661	ACGAGAAAGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAA	720	XX
QY	721	ACCAACGTCATRACTCATTTACGATGATGATGATGAGGACTTCACCC	780	DT
Db	721	ACGAACTGTCACCTGATGATGATGAGGACTTCACCC	780	XX
QY	721	ACCAACGTCATRACTCATTTACGATGATGATGAGGACTTCACCC	780	DE
Db	721	ACGAACTGTCACCTGATGATGATGAGGACTTCACCC	780	XX
QY	781	GTCTTGTACAGAACTCGGACTTCATCGCTGCGTCAAGGCCAGGATTTG	840	Antisense oligonucleotide: groE; groEL; groES; inhibitor; growth;
Db	781	GTCTTGTACAGAACTCGGACTTCATCGCTGCGTCAAGGCCAGGATTTG	840	microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
QY	841	GATCGCTGTAAGCTATGCTGAGACATTTGACAGTGTGATGCTGAGCT	900	Streptococcus pneumoniae; Staphylococcus aureus; Pseudomonas aeruginosa;
Db	841	GATCGCTGTAAGCTATGCTGAGACATTTGACAGTGTGATGCTGAGCT	900	antibacterial; antiviral; antiproliferative; antisense therapy;
QY	901	GAAGATCTAGACTGTGTTAAAGATCTCATGACGACGCCCTTGACAG	960	microbial infection; ds.
Db	901	GAAGATCTAGACTGTGTTAAAGATCTCATGACGACGCCCTTGACAG	960	XX
QY	961	ATTCAGTTGATTAAGTAGGACAGCTAATGTTGAGGTTCAGGAAGTGT	1020	Streptococcus pneumoniae.
Db	961	ATTCAGTTGATTAAGTAGGACAGCTAATGTTGAGGTTCAGGAAGTGT	1020	XX
QY	1021	GCTAACCGTTGCTGTGTTGAAAGATGGACATGAGCTTGACCTGACCG	1080	PN WO20013662-A2.
Db	1021	GCTAACCGTTGCTGTGTTGAAAGATGGACATGAGCTTGACCTGACCG	1080	XX
QY	1081	GAAGACTTACAGAACTTGGCAAAATGGTGTGTTGAGGGAAATCTGAG	1140	PD 25-MAY-2001.
Db	1081	GAAGACTTACAGAACTTGGCAAAATGGTGTGTTGAGGGAAATCTGAG	1140	XX
QY	1141	GTCTTGTACAGAGGACGGTTAAAGAAATGAACTTCGATTTGAGGTCT	1200	PF 20-NOV-2000; 2000WQ-CA01347.
Db	1141	GTCTTGTACAGAGGACGGTTAAAGAAATGAACTTCGATTTGAGGTCT	1200	XX
QY	1201	ACAGSGCAGCCCTGAGGAGGATCTTGTGTTGGGGACGACACTTAA	1260	PR 18-NOV-1999; 9918-0166249.
Db	1201	ACAGSGCAGCCCTGAGGAGGATCTTGTGTTGGGGACGACACTTAA	1260	XX
QY	1261	ATTTGAAAGTGTGAGGCTCTGAGGGTGTGACTGAGCTTACATGTTG	1320	PA (GENE-) GENESENSE TECHNOLOGIES INC.
Db	1261	ATTTGAAAGTGTGAGGCTCTGAGGGTGTGACTGAGCTTACATGTTG	1320	XX
QY	1321	CTTCGTCCTAGAGGCTCTGAGGGTGTGAGGGTGTGACTGAGCTTAC	1380	PT Wright JA, Young AH, Dugourd D;
Db	1321	CTTCGTCCTAGAGGCTCTGAGGGTGTGACTGAGCTTACATGTTG	1380	XX
QY	1381	GTGATGCTGAGTGTGAGGTTATGGTGTGAGGTTATGGTGTGAGGTT	1440	DR
Db	1381	GTGATGCTGAGTGTGAGGTTATGGTGTGAGGTTATGGTGTGAGGTT	1440	XX
QY	1441	GGTGGGGTGTACGATTAATCAGTGTGATGATGATGATGATGATGATG	1500	XX
Db	1441	GGTGGGGTGTACGATTAATCAGTGTGATGATGATGATGATGATGATG	1500	Novel antisense compounds targeting nucleic acid encoding groEL or
QY	1501	CTTCAGAACTCTGAGGTTATGGTGTGAGGTTATGGTGTGAGGTT	1560	PT gross gene of microorganism, which hybridizes with and inhibit
Db	1501	CTTCAGAACTCTGAGGTTATGGTGTGAGGTTATGGTGTGAGGTT	1560	PT expression of the genes, useful to inhibit growth of microorganism
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	PT having the genes .
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	XX
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	PS Disclosure: Fig 6; 110PP; English.
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	XX
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	The present invention specifically claims AH56360 to AH56822 which are
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	antisense oligonucleotides to nucleotide sequences encoding groE. More
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	generally, antisense compounds (1) comprising antisense oligonucleotides
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	5-50 bases targeted to a nucleotide sequence encoding groEL (heat
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	microorganism, where the antisense compound is complementary to GL or
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	GS of a microorganism and specifically hybridises with and inhibits the
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	expression of GL or GS, is claimed. (1) have antibacterial, antiviral
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	and antiproliferative activities and can be used in antisense therapy
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	and for inhibition of expression of groS or groEL. (1) are useful for
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	inhibiting expression of GL or GS in cells or tissues <i>in vitro</i> . (1) are
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	also useful for inhibiting the growth of a microorganism, or inhibiting
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	the expression of GL or GS gene in a microorganism (a bacterial cell or
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	a virus) having a GL or GS gene which involves administering to the
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	microorganism or to a cell infected with the microorganism. (1) (1) are
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	also useful for treating a mammalian pathological condition mediated by
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	the microorganisms which involves identifying a eukaryotic organism
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	having a pathological condition mediated by microorganisms having a GL
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	or GS gene and administering (1) such that the growth of microorganism
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	is inhibited. The antisense compounds are utilised for diagnostics,
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	therapeutics, prophylaxis and as research reagents and kits, e.g., to
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	prevent or delay microbial infections in humans. They are also useful as
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	molecular weight markers. AH56362 to AH5637 and AH5633 to AH5684
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	represent PCR primers for groE genes which are used to AH56854
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	exemplification of the present invention. AH5685 to AH56870 represent
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	groE nucleotide sequence given in the present invention.
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	XX Sequence 2107 BP; 650 A; 400 C; 508 G; 549 T; 0 other;
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	Query Match 63.2%; score 1036; DB 22; Length 2107;
Db	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	Best Local Similarity 77.5%; Pred. No. 5e-261; Mismatches 365; Indels 0; Gaps 0;
QY	1561	AAACCTGAGACCACTAGGCCAGCCAGCATGGCAGCTTGACAGCTG	1620	Matches 1255; Conservative

QY	1	ATGGCAGAAAGAATCAATTTCAGCGATCGCGCTCTGCCATGTCGGGGACTGT	60	Db	1565	GAATAATGCAAGACGCTGGCCAAATGTCAGGGTGTACCGGTATTAAGGTGGA	1624
Db	485	ATGTCAGAAAGAATTAATTAATTCATCGATGCGCTGCACTGTCGCGGGCTCGAT	544	QY	1141	GCTCCACAGAGAGCTTAAGAAGTAACACTGCGATGAGCTTGTGCTCTGCT	1700
QY	61	ATGTTAGCAGATACCTCAAGAACGCTGCTCTAAGGCCCAATGTCGCTCTGAA	120	Db	1625	GCGCAACTGAACTGATGAGCTGAGAAATGACCTCGCCATGAGATGCGTCACGCT	1684
Db	545	ATCCCTGCGAGAATCTTAAGGACACTTGTGAGGACCAAAAGGTGCGCAATGTCGAA	604	QY	121	AAAGCTTGGTCCCTTAATTAATGAGCTTGTGAGGAACTTGTAAAGATTCGA	180
QY	605	AAATCATTGTCACATGTCATGATGACCAATGAGCTTGTGAGGAACTTGTAAAGATTCGA	664	Db	1685	ACTGTCAGCTGAGTGTGAGAAGTAATGACCTCGCCATGAGATGCGTCACGCT	1744
Db	605	TTAGAGACCATTTGAAACATGGAGCAAAATGTCGAGGCTGACTATGCGCAGAATTCGA	240	QY	181	TTAGAGACCATTTGAAACATGGAGCAAAATGTCGAGGCTGACTATGCGCAGAATTCGA	180
Db	665	TTAGAGACCATTTGAAACATGGAGCAAAATGTCGAGGCTGACTATGCGCAGAATTCGA	724	Db	1745	ATTCACGCTGTGTAACCTGGTAAATTGACAGAGATGAGCTGAGAGCTATAGGT	1004
QY	241	ATGATATTCGCTGATGGACACTACTGCAACAGCTTGTACACRAGCAGATGTCAT	300	QY	1321	CTTCGCTCTAGAGGCCATGCTCAATTGCTTAAATGCTGGTACGAGGCTCC	1380
Db	725	ATGATATTCGCGAGTGTGACCGACTATGAGCTGCAACACTCTGACCGCAAGCTGTCGCT	784	Db	1805	CTCCGCTTTGAGAACCGTGTGCAATGTCACAGCAGGATTGAGGCT	1664
QY	301	GRAGGACTAAATGAGCTGACGAGGTGCTAATCAGTGTACCTCGTGGATGAA	360	QY	1381	GRAGTATGACAGATGAAACAGGCCCTCAGAACAGGTTAACTCGAGGTT	1440
Db	785	GRAGGAAATCAGAACCTCACAGAGGTCATGAACTCGTGTATTCGGGATGAA	844	Db	1865	ATGTTATGATGTTGAAAATGCTGAGGTTAAGGTTAACCGACAACTGGC	1924
QY	361	ACAGAACAGCAGCACAGCTTGTAAAGACGCTGAAAGGCTATGCTCACCTGAG	420	QY	1441	GATGGGTTGATGATTAACAGGAACTGACCCCTGTGCAAGTAACAGATAGCG	1500
Db	845	ACAGCAGTGTGCCGAGCAGTGTGAGTTGAAACACGCCATCCGTGCAATGAA	904	Db	1925	GATGGGTTAACATGATGATGACGATGTCAGGTTGATCCAGTAAAGTGTGCA	1984
QY	421	GAAGCTTGTCTCTGCTGCTGAGTATCAGCCTGCTGAAAGATGAGACTATC	480	QY	1501	CTTCAAATGCACTTCGAGCTGAGCTTATGACAGAACGCTTGTGAA	1560
Db	905	GAACATCTGCTGAGTTCGACCGTATTCGCGCTGTTGAAACACGCCATCCGTGCAATGAA	964	Db	1985	CTACATGATGAGCTGTCAGGTTGACACGAGCTGTCAGTCCGCAAT	2044
QY	481	TCAGAGCTATGGAGCGTGTGGCAACGATGGTGTATGACCTCCAGAGATCGGGT	540	QY	1561	AAACCTGACCACTGGCCAGGCCAGCAGTGTGAGCAGTATGATCCAGAATG	1620
Db	965	TCTCAGAATGGAAAGATGGTGTGAAAGACGCTGTCACCTCCAGAGATCGGGT	1024	Db	2045	AAACCGAACGCTAGCCCCAGCTCCAGCTGATGGTCAAGATATGGCGGAGATG	2104
QY	541	ATGAAACAGAACTGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGCTCAA	600	RESULT	13		
Db	1025	ATGGAACAGACAGCTGCTGAGTGTGAGCTGAGCTGAGCTGAGCTGCTCAA	1084	AAV5210			
QY	601	TACATGGTCAGACGACATGAAATGAGCTGAGCTGAAACCATWATCTTATC	660	ID	AAV5210		
Db	1085	TACATGGTCAGACGATAGGAAANATGGGGTGTGAGCTGAAATCGTACATTGTT	1144	XX			
QY	661	ACGGATTAAGAGTGTCAACATCCAGACATTTCCACTACTTGTAGGAGTCATA	720	AC	AAV5210;		
Db	1145	ACAGACAGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAA	1204	DE			
QY	721	ACGACCGTCATRACTATGAGTGGTGTGGAGTACACTCCACCTT	780	XX			
Db	1205	ACGATGTCGACACTCTGATGATTCGGATGATGGATGGGGAGCTCTCCACCT	1264	XX			
QY	781	GTCCTGACAGATCGGGTACTTCATGGGTGCTCAAGGCCAGGATGGT	840	KW			
Db	1265	GTTTGACGACAGATTCGGATGATGGATGGGGAGCTCTCCACCT	1224	streptococci pneumoniae; S. pneumoniae; genome; diagnosis; assay;			
QY	841	GATCGCTGTAAGATGCTGAGACATGCTACTCTGACAGGTTGACAGTACA	900	OS			
Db	1325	GACCGTGCAGACGCCATCTGAGATATCGCCATTACAGGCCAGCTATCACA	1384	XX			
QY	901	GAGGATCTGAGTGTGAGTAAAGATGCTACAGACGCCCTGAGCTGTTGAA	960	streptococci pneumoniae.			
Db	1385	GAGACCTGSGCTGAGTAAAGATGCTACAGACGCCCTGAGCTGTTGAA	1444	XX			
QY	961	ATTACAGCTGATGAGATGAGCTAATGTTGAGGTCTGAGGAGTCAGAGT	1220	PR			
Db	1445	GTGACCTGAGCAAGATGAGCTGAGCTGTTGAGGAGGCGAGGAAATCTGAGGAA	1504	XX			
QY	1021	GTGACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT	1080	PA	(HUMA-) HUMAN GENOME SCI INC.		
Db	1505	CTTCACCGGTGTTGCGGTTATCAAGCTCAATCGCAACTACACTCTGAGT	1564	XX			
QY	1081	GAAGAACTACAGAGACGTTGGCGAAATGAGCTGAGCTTATCAAGTAGGA	1140	PI	Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;		
			PI	Kunsch CA, Rosen CA;			
			XX				
			PR				
			XX	31-OCT-1996; 95US-002960.			
			PA				
			XX	WPI: 1998-27225/24.			
			PT				
			PT	Computer-readable medium with recorded Streptococcus pneumoniae			
			PT	polynucleotide sequences - useful in diagnostic kits and assays, and			
			PT	pharmaceutical compositions and vaccines for Streptococcus			
			XX	pneumoniae			
			PS	Claim 1; Page 628-631; 1409PP; English.			
			XX				

CC
CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV5214 to AAV524) recorded on 1, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV5214 to AAV524) are genomic fragments from *streptococcus pneumoniae*. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the *S.pneumoniae* genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the *S.pneumoniae* genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the *S. pneumoniae* genome of commercial importance, or expression modulating fragments of the *S. pneumoniae* genome. Products from the present invention can be used in diagnostic kits and assays, and pharmaceutical compositions and vaccines for *S. pneumoniae*.

SO

Sequence 5365 BP; 1654 A; 960 C; 1082 G; 1669 T; 0 other;

Query

Match, Best Local Similarity 77.4%; Pred. No. 1, 9e-260; Length 5365;

Matches 1254; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

QY 1 ATGGCAGAAGAACATCAATTTCGACAGATGGCGCCTGAGCTTGGTAAAGGGCATGTGTTCTAA 60

Db 278 ATGCTTACAGAACGAAATTAATTTCTTCAGATGCCCTTCAGCCTTGCTGTTGCGAT 337

QY 61 ATGTTACGAGATTCGGCTCAAGTAACTGGCTTGGTCTTAAGGGCATGTGTTCTAA 120

Db 338 ATGCTTACAGAACGAAATTAATTTCTTCAGATGCCCTTCAGCCTTGCTGTTGCGAT 397

QY 121 ATAGCTTGTGTTCTCCCTTAATTAATCTATATAGCTGGGGTACCATCTTAAAGATGCGAA 180

Db 398 ATGCTTACGAGATTCGGCTCAAGTAACTGGCTTGGTCTAAAGGGCATGTGTTCTAA 457

QY 181 TTGAAAGATCTTGGAAACATGGGACAAATGGCTTGAGTGCTCTAAACC 240

Db 459 TTGGAAGAACCTTTGATGAAATAGCTGGCTTAAGTGTAGTATAGAAGTAGCTCTAAACC 517

QY 241 ATGATATATGCTGTGATGGACCACTACTCACAAGCTTGTACGAAAGCCATGTGTT 300

Db 518 ATGATATATGCTGTGATGGACCACTACTCACAAGCTTGTACGAAAGCCATGTGTT 577

QY 301 GAGGAGCTAAATGAGAGCAGGGCTTAATCCAAATGGTAAATGCCGAGCTAA 360

Db 578 GAGGAGCTAAATGAGAGCAGGGCTTAATCCAAATGGTAAATGCCGAGCTAA 637

QY 351 ACAGCACACGAAACAGCTGTGAGGCCATGTGTCACCTCTGCTGCAAG 420

Db 638 ATGCGATGTCGCGCAGCAGCTGTGAGCTTGGTAAACACGCACTCCGTTGCAATCA 697

QY 421 GAGGAGCTTGTGCTGAGTCGCTGGTCACTATCATCACGCTGTGAAAGATGAGGATTC 480

Db 698 GAGGAGCTTGTGCTGAGTCGCTGGTCACTATCATCACGCTGTGAAAGATGAGGATTC 757

QY 481 TCGAGAGCTTGTGCTGAGTCGCTGGTCACTATCATCACGCTGTGAAAGATGAGGATTC 540

Db 758 TCTGAGGAGCTTGTGCTGAGTCGCTGGTCACTATCATCACGCTGTGAAAGATGAGGATTC 817

QY 541 ATGGAACAGAACCTTGTGAGGATCAATTGTGCGCTTGTGCTGCAAA 600

Db 818 ATGGAACAGAACCTTGTGAGGATCAATTGTGCGCTTGTGCTGCAAA 877

QY 601 TCTGAGGAGCTTGTGCTGAGTCGCTGGTCACTATCATCACGCTGTGAAAGATGAGGATTC 660

Db 878 TCTGAGGAGCTTGTGCTGAGTCGCTGGTCACTATCATCACGCTGTGAAAGATGAGGATTC 937

QY

661 ACCGATTTAAAGTGTCACACATCCAAAGACATTGTGCGACTACTTGAGGAATCTAA 720

Db 938 ACAGACAGAAATTCCATTCACGAACTCTGCGACTCTTGAGAACTTC 997

QY 721 ACCAACGTCCTACTCTATTATGCGAGCATGTGATGGATGGTGAAGCTTCACCTT 780

Db 998 ACCAATGTCGACTCTGTGTTGTTGTTGCGAGCTTCACCTT 1057

QY 781 GCTGAGACAGATGTGGTACTTGTGAGATGTGGTGTGTCAAAGCAGCAGATGGT 840

Db 1058 GTTTGTGACAAAGATTGTGAACTCTCAAGCTGAGTAGTAGCTGAGCAGCAGCCTT 1117

QY 841 GATGCCGCTTAAGCTATGCTGTGAGACATGTGCTCTTGAGCTGAGCTGTTGATCA 900

Db 1118 GACCGGCGCAACCTGCTTGAGATATGCGCATTCAGCCGGACATGATCA 1177

QY 901 GAGGAGCTGGAGCTGAAATTAAGATGTCACATGACACCCCTGGACAGCCTG 960

Db 1178 GAGGAGCTGGCTGAGCTGAGTAGCTGAGATGAGCTGAGCTGAGCTGGT 1237

QY 961 ATTACAGTTGATGATGAGCTACAGCATGAGTGTGAGGTTGAGGTTGAGCTT 1020

Db 1238 GTGACGGTGACAAAGATGACAGCTGAGCTGAGCTGAGCTGAGCTGGT 1297

QY 1021 GCTAACCTTGTGACTGTGTTAAATGCAATTGACATTAAGACACAACTCTGTGACCT 1010

Db 1298 TCTCACCGTGTGCGCTTGTCAAGTCACATGCAACTACACTCTGTGATTCAGCT 1357

QY 1081 GAAACACTACAGAACTGTGCGAATATGGCTTGCGGCGTGTGTTGCTGTATCAAGTGA 1140

Db 1358 GAAAAATGCGAAAGAACGCTGCGCAATATGTCAGGAGGTGTTAGGGTTTAATAGTTGA 1417

QY 1141 GCTCCAAAGAGACAGCTTAAGAAAGATGAACTCGATGTGAGATGCTGTTAAGCT 1200

Db 1418 GCGCAACTGAAACTCGATGTGAGAAATGAACTCGATGTGAGGTGTTAGGGCTTCAAGCT 1477

QY 1201 ACACGTGAGCGTGTGAGAAGAGTGTGAGCTGAGGAGTGTGTTGGGGGGGAGACACTTAA 1360

Db 1478 ACTGCTGAGCTGTTGAGAGCTGAGGAGTTGGTGCAGGGGGGAGACACTCTGGCTG 1337

QY 1361 ATGAAAGATGAGCTTGTGAGCTGAGGAGTGTGAGCTGACTGCTAACATGTTG 1120

Db 1538 ATTCGACTGTGTTGCTACCTTGAAATGAGATGAACTCGATGTGAGATGAGCTTAA 1597

QY 1321 CTGCTCTCTAGAGAACCTGAGCTGAGTGTGAGTGTGAGCTTAAATGCTGGTACGAGGOTCC 1380

Db 1598 CTGCTCTCTAGAGAACCTGAGCTGAGTGTGAGCTGAGTGTGAGCTTAAATGCTGGTACGAGGATCT 1657

QY 1381 GTAGTTATGACAGTGTGAAACACGCCCTGCGAGACAGGTTATGCTGGTACGAGT 1440

Db 1658 ATCGTATTCGATGCTGTGAGAAATGCTGAGCTGAGTGTGAGCTTAAACGCGACTGGC 1717

QY 1441 GAGGGGTGTGATGATTAACAGGAACTATGAGCTGAGCTGAGCTGAGCTGAGC 1500

Db 1718 GAGGGGTGTGATGATGAGCTGAGCTGAGTGTGAGCTGAGCTGAGCTGAGCTGAGC 1777

QY 1501 CTGCAATGCACTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGC 1560

Db 1778 CTGAAATGCACTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGC 1837

QY 1561 AACCTGACCGTAGGCCGCGCAGCAATGCCGAGCTGAGCTGAGCTGAGCTGAGC 1620

Db 1838 AAACCGAGACCTAGGCCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGC 1897

RESULT 14

ARMS659

ID AHS6859 standard; DNA: 2401 BP.

AC AHS6859;

XX

DT 06-SEP-2001 (first entry)

DE	S. pneumoniae groE operon nucleotide sequence SEQ ID NO:5.
KW	Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth; microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis; Streptococcus pneumoniae; Staphylococcus aureus; <i>Pseudomonas aeruginosa</i> ; antibacterial; antiviral; antiproliferative; antisense therapy; microbial infection; ds.
KW	XX
OS	Streptococcus pneumoniae.
XX	XX
PN	WO200136625-A2.
XX	XX
PD	25-MAY-2001.
XX	XX
PF	20-NOV-2000; 2000HO-CA01347.
XX	XX
PR	18-NOV-1999; 99HS-0166249.
XX	XX
PA	(GENE-) GENESENSE TECHNOLOGIES INC.
XX	XX
PI	Wright JA, Young AH, Dugourd D;
XX	XX
DR	WPI: 2001-355633/37.
PS	Novel antisense compounds targeting nucleic acid encoding groEL or groES gene of microorganism, which hybridize with and inhibit expression of the genes, useful to inhibit growth of microorganism having the genes.
PS	Disclosure: FIG 5; 110PP; English.
CC	The present invention specifically claims AAH56368 to AAH56832 which are antisense oligonucleotides to nucleotide sequences encoding groEL. More generally, antisense compounds (1) comprising antisense oligonucleotides of 5-50 bases targeted to a nucleotide sequence encoding antisense oligonucleotides (heat shock protein (HSP60) (GL) and groES (HSP10) (GS) gene from a microorganism, where the antisense compound is complementary to GL or GS of a microorganism and specifically hybridises with and inhibits the expression of GL or GS, is claimed. (1) have antibacterial, antiviral and antiproliferative activities, and can be used in antisense therapy and for inhibition of expression of groES or groEL. (1) are useful for inhibiting expression of GL or GS in tissues <i>in vitro</i> . (1) are also useful for inhibiting the growth of a microorganism, or inhibiting the expression of GL or GS gene in a microorganism (a bacterial cell or a virus) having a GL or GS gene which involves administering to the microorganism or to a cell infected by the microorganism. (1) are also useful for treating a mammalian pathological condition mediated by the microorganisms which involves identifying a eukaryotic organism having a pathological condition mediated by microorganisms having a GL or GS gene and administering (1) such that the growth of microorganism is inhibited. The antisense compounds are utilised for diagnostics, therapeutics, prophylaxis and as research reagents and kits, e.g., to prevent or delay microbial infections in humans. They are also useful as molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56834 represent PCR primers for groE sequences which are used in the amplification of the present invention. AAH5655 to AAH56870 represent groE nucleotide sequence given in the present invention.
SQ	Sequence 2401 BP; 743 A; 459 C; 568 G; 631 T; 0 other;
Query Match	62.9%; Score 1029 5; DB 22; Length 2401;
Best Local Similarity	77.2%; Pre 2.5e-259;
Matches	1251; Conservative 0; Mismatches 369; Indels 0; Gaps 0
OY	1 ATGGCAAAAGAGATAAATTTCGAGATGGCGCGCCGAGGCGAGTGTAT
DB	61 ATGGTAGGAGATACCGTAACTAACGCTTGCTTAAGGGCGATGTGCTGAA 60
OY	61 ATGGCAAAAGAGATAAATTTCGAGATGGCGCGCCGAGGCGAGTGTAT
DB	679 ATCCCTGGAGACAGCTGTAAGTAACTAACGCTTGCGACCAAAGATGCGATGCGCTGAA 738
OY	121 AAAGCTTGTTCGCCCTAATCTATAGCGGGTAACTCTCTAAAGATGCGAA 180

Db	739	AAGTCATCTGTTTACCCCTGTTACCAATGAGGTGAGCATTCGCAAGAATCGAA	798
Qy	181	TTAGAGATCATTTGAAACATGGGCAAAATGGTGTGAGTGGCTCTRAACC	240
Db	799	TGGAACGACTTTGAAATATGGTGTGCAACTTACGAAATAGCTCTRAAAC	659
Qy	241	AAGCATTTGGTGTAGGGGACTACTGCCAACATPTGACAGCAGCCATGTCAT	300
Db	859	AATGATATCGCAGGTTGGGACTAGCTGCAACTCTGACGCAAGCTGCGCT	918
Qy	301	GAAGCTAAATAATGTCACRCGGCTAATCCAAATGGTACCTGAGTAAAG	360
Db	919	GANGAACATCAAAAGTCACACAGCTGCAATCGACATGCGTGGGTTGAA	978
Qy	361	ACGCAACAGCACGCGTGTGAAAGCCATTGTCACCGTATCTGCANG	420
Db	979	ACAGCAGTGGCCGAGCAGTGTGAAACACGCATCCCTGTCGCAATAA	1038
Qy	421	GAAGCTTATGCTCGAGGCGCAGTATCAGTCACTCGCCTGAAAGAAGT	480
Db	1039	GANGCTTCTCAGTGCACCGTATCTCGCTCTGAAAGTGGGTTGAGTAC	1098
Qy	481	TCGAAGCTTGGAGCCTGGCAGCTGGTGGTGTGATTCATGAGAATTC	540
Db	1099	TCGAGAACGATGAAAGTGGCAAGCGGGTGTATCCACCATCGANGATC	1158
Qy	541	ATGGAAACGACACTGAGTGGTAAAGCATGCATGCAATTGACCTGGTAC	600
Db	1159	ATGGAAACGAGCAGTGTGAGTGGTAAAGAAGTGGACTTGGCTGTTAC	1218
Qy	601	TACATGTCAGCAATGAAATGGTGGTCAAGAAGCAGTGGTACCTTAC	660
Db	1219	TACATGTCAGTGTGAAAGAATGGTGGGCGGACTCTGAAATTCGTTA	1278
Qy	661	ACGATTAAGAAATGTCGAACATCCAAAGACATTGCCCACATCTGGAA	720
Db	1279	ACGAGCAAGAAATTCGAAATTCGAAAGAAATCTGGCCACTTGGAAAGCT	1338
Qy	721	ACCAACCGTCATRACTCATATGTCAGATGAGTGGGAGGTTGAGACTT	780
Db	1339	ACACATGTCACCTCTGATATTGCGATGTTGATGATGCGGGGTTGAGT	1398
Qy	781	GTCTTGAAAGAATTCGTTGATCTCATGTTGTTGCTGTCAGAGCCAGAT	840
Db	1399	GTGTTGAAAGATTCGTTGGAACCTTCACGTTGAGCTGAGTCAGGACCT	1458
Qy	841	GTCTCGTGAAGCTGAGCTGAGACATGTGTCTGAGCTGTGAGTGTCA	900
Db	1459	GACCGTCGCAAAACCGTGTGAGATTCGCCCACCTAACAGCGGAGCT	1518
Qy	901	GAGGATCTAGGACTGTGATAAAGATCTCATGACAGCCCTGGACAGCT	960
Db	1519	GRAGACCTGTTGCTTGTGAGATGGCGAACATGAGCTTGTGACCTG	1578
Qy	961	ATTACAGTGTGATAAGATGAGCTGAACTGCTGAGTGTGAGGTTGAG	1020
Db	1579	GTGACCGTGTGACAAATATCGCGTTATGGAGGGTGCAGGAATTCGAGG	1638
Qy	1021	GCTAACCGTATCTGATTAATGCAATGAAACACACCTCTGACTGTGAC	1080
Db	1639	TCTCACCGGTTGGGTATCACTCTCAATCGAACACTACACTCTGATTC	1698
Qy	1081	GRAAACTTCAGAACTGTTGGGAATTAGCTGTGGTGTACTCTGTTAC	1140
Db	1699	GRAAATTGCAAGAACGCTGCGCAATTGCACTGGTGTGGTTAGGGTTA	1758
Qy	1141	GCTCCAACGAGACGCTTAAAGAAATGAACTTCGATGGGGTCTAACT	1200
Db	1759	GCGGACTGTGAACTGAGTGTGAAAGATGAACTGGATGAGCTGCCTAC	1818
Qy	1201	ACACCTGAGCGGTTGAGAGATATGGTGTGTTGGGGACGCACTTAACT	1260

Query Match 58 3%; Score 954 2; DB 24; Length 2365589;
 Best Local Similarity 75.2%; Pred. No. 2.2e-38; Matches 1190; Conservative 0; Mismatches 393; Indels 0; Gaps 0;

QY 1321 CTCGCGCTCTAAGAGCTGTCGAATGCTGACTGAGCTACATG 1320
 Db 1879 ATTCAGCTGAACTACTACTCTGGATTGAGCAACAGAGCTATATGT 1938
 QY 1381 GATGTTATGACAGTGAAGAACAGCCCTGACGACAGGTTATG 1380
 Db 1939 ATTCGGCTTGTGAGAACCGCTGTCAAATTGTCACAAAGCAGGATTGAGATCT 1998
 QY 1501 CTCAAATGCACTCTGTCAGCTTGTGACAGTGTGGCAAGCT 1440
 Db 1999 ATCGTATGCTGTTGAAKAAAGCTGAGCTGTGTTATAGTTAACCGCAACTGC 2058
 QY 1441 GAGTGGTGTGATGTTAAACGGATCTTGCCTGTCAAAGTACAGATAGCC 1500
 Db 2059 GGTTGGTTAACATGTTGTTGACAGGTTCTGTCAGGTTAATGTTGTCAGCC 2118
 QY 1561 AACCTGAAACCTAGCCAGCCAGCAGTGTGACAGGAGTGTGTCAGT 1620
 Db 2119 CTACAAATGCACTCTGTCAGCTGACAGTGTGACAGGAGTGTGTCAGT 2178
 Db 2179 AACCGAGAACCTAGGCCAGCAGCTAACGATGTTGACAGGAGTGTGTCAGT 2238

RESULT 15

AB0521
 ID AB0521 standard; DNA; 2365589 BP.
 AC AB0521;
 XX
 DT 16-MAY-2002 (first entry)
 DE Genomic sequence of Lactococcus lactis Ii1403.
 KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese; ds.
 OS Lactococcus lactis Ii1403.
 XX
 PN FR2807446-A1.
 PD 12-OCT-2001.
 XX
 PF 11-APR-2000; 2000FR-0004630.
 XX
 PR 11-APR-2000; 2000FR-0004630.
 XX
 (INRG) INRA INST INAT RECH AGRONOMIQUE.
 PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 DR WPI: 2002-04-3418/06.

PT New nucleotide sequence useful in the identification of Lactococcus lactis and related species -

PS Claim 1; SEQ ID 1; 250PP; French.

XX
 CC The present invention is related to a Lactococcus lactis nucleotide sequence (AB0521) and related proteins (AB53100-AB5621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

CC Note: The sequence data for this patent is based on equivalent patent WO20017334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at http://wipo.int/patents/pct_sequences.

XX
 Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;

Query Match 58 3%; Score 954 2; DB 24; Length 2365589;
 Best Local Similarity 75.2%; Pred. No. 2.2e-38; Matches 1190; Conservative 0; Mismatches 393; Indels 0; Gaps 0;

QY 1 ATGCCAAAGAAATCAATTTCAGGAGTGGCGCTCCATGGGGAGTGT 60
 Db 398897 ATGCAAAAGATATTAATTTCAACTGAGVNGCAGTGAAGCAGTGGATGAT 398956
 QY 61 ATGTTAGAGATACGGCTCAAATAGCTGGCTGRCCTAAGGGCAATGTCCTGAA 120
 Db 39857 ATTCGGTGTACAGTAAACACACCCCTGGACRAGTGTGCAATGTTGAA 399016
 QY 121 AAAGTTTGGTCTCCCTTAATTAATGAGGGTAACTCTCTAAAGAGATGAA 180
 Db 399017 AAATCTATGTTACCTTTAATTAATGAAACGATGGCTAACGTTGCAAGATGAA 399076
 QY 181 TTAGAGTCATTGAAACATGGGAAATTTGGTCTGAAGCTGTTGAGCTGTGTTAAC 240
 Db 399077 CTTAAGATGTCATTGAAATATGGAGCTAACTTGTTGAGCTAACAGTGTGTTAAC 399136
 QY 241 AATGATATGTTGGGATGGGAGCTACTGCACTGAGCTTGTACAGCATGTTCA 300
 Db 399137 ATATATGGAGGTGAGCTACACACAGGGACAGTGTGACACAGCTATGTTG 399196
 QY 301 GAAGACAAAGAAATGTCACAGCTGCTTAATGTCAGTGTGAGCTGAA 360
 Db 399197 GAAGTTTAAATGTTAACGAGTGTGAGCTGAAATCCCTGTTGAGGATGAA 399256
 QY 361 ACACAAACAGAACAGCTGCTGAGCTGAA 420
 Db 399257 CTGGCTCTGAAACAGCTGCGTCAATTAAAGAGATGCACTTCTCCCGTAA 399316
 QY 421 GAAGCTATGTCAGGTCGGCCASTATCATCACGCTGAAAGTTGAGATVATC 180
 Db 399317 TCAGCAATTGCGCAGTAGTCACCTTTCATCACCTAGTGAAGAAGTGGTGTAA 399376
 QY 481 TCAGAGCTATGGAGCCTGGGGCAACCATGTCGTTACATGAGCTCCAGT 540
 Db 399377 TCTGATCCAAATGGACCTGGTCTGACGAGTATCACCTGAAATCCAGT 399436
 QY 541 ATSGAACAGAACGACTGTGAGTGTGAGGCTGCAATTGACCTGTCIA 600
 Db 399437 ATGCAAACTGACCTGAGCTGTTGAGGATGTCAGTGGTGTAA 399496
 QY 601 TCTAGCTCAGCATGAAATGTTGACGCTGAAACCCATTTCATTCAT 540
 Db 399497 TATATGTTCTTAATACAGAAAGATGTTGATGATGAAACCTTATCTTAA 399556
 QY 61 ACGGATAAAAGTGTCAACATCCAGCTTGTGACACTTGAGGACTCTAA 720
 Db 399557 ACCGAAACAAATCTAACATCAGAAATTTACGGCTCTGACAAATCTGAA 399616
 QY 721 ACCAACCGCAATTACATCATATGAGATCATGGATGGTGAAGCACTCCACCT 780
 Db 399617 ACAAATGTCACCTCTTATGTTGAGCTGATGATGTTGAGAACGCT 399676
 QY 781 GCTTCACAGATCTGTGACTTTAATGTTGCTGTCAGTGTGAGCTGCAACGCT 840
 Db 399677 GTCCTAAAGTTAACGCTTGTGAGCTGTTGAGCTGAAAGCAGTGT 399736
 QY 841 GATCGTGTGAACTATGCTGAGACATGCTACTGAGGTTGAGCTGAGCTGAA 900
 Db 399737 GATCGTGTGAACTATGCTGAGACATGCTACTGAGGTTGAGCTGAA 399796
 QY 901 GAGGCTGAGCTGAGCTGAAAGTGTGACAGCTGAGCTGAGCTGAGCTGAA 960
 Db 399797 GAGAAGCTGTTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAA 399856
 QY 961 ATTAGCTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAA 1020
 Db 399857 GAACTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAA 399916

OY	1021	OCTAACCGTATGCACTGTTAATGCAATTAGAACACAACCTCTGACTTGTACCGT	1080
OY	1081	GAACAACTACAGAAGCTTGGGAATATTAGCTGTGTGTAGCTGTATTCAGAATGGA	1140
Db	399977	GAACAAATTACAGAACGCTTGTGCAAAATTAGCTGTGTGTGTTGCGTTGAATGTTG	400036
OY	1141	CCTCCACAGACAGACGTTAAAGAAATGAAACTTGGCATTTGGAGATGCTCAATCT	1200
Db	400037	GCTGCAACTGTGACAGCTCAAGAATGAAACTCTGTGTGAGATGACTTAATGCA	400096
OY	1201	ACAGCTGTCAGCGGTGAGAAGTGTACCGTGTGCGGPGGAGACGACTTATCGGT	1260
Db	400097	ACAGCTGCAAGCGGTGAGGAGGTATGTCTGGTGTGACGACTGTAACTCT	400156
OY	1261	ATTCAGAAAGTGTGACGCTTCACTGTGAGGCGATGAGTGTGCTGACATCTG	1320
Db	400157	ATTCGTGTTGATAACTTGTGAGGAGGATTTCAACAGGTATTAACAGTT	400216
OY	1321	CTTGTGTCAGAAGAGCTGTACCTCAATGCTTAAATGCTGGTGTGAGGTCTC	1380
Db	400217	CGCGCTCTGTGAGAACCTGTCAATTGCTGCAATTCGPGCCATCTGAGATGAGGTC	400276
OY	1441	GACGGGTGTATGATTAACAGAACGAAATCATGACCCGTCAAGTACAGATCGG	1500
Db	400337	CAATGGGTAAATGATGAGAAGAAGAATGACCTGCAAAAGTACTGTGTGCACTGT	400396
OY	1501	CTTCAAATGAGCTCTGTGACTGTCTTATTTGACACAGAACAGTGTGTCAAT	1560
Db	400397	TGGAAACAGGCTCTGTGTGTGTTAATTTGACTGTGAGTAGTGTCAAT	400456
OY	1561	AAACCTGAGACGCTACGCCACG	1583
Db	400457	AAGCCAGACGACGCCAGCTGCCAG	400479